



Docket No.: MBI-0010

#231
11-7-02

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

RECEIVED

OCT 31 2002

In re Application of: Heard et al.

Title: DISEASE-INDUCED POLYNUCLEOTIDES

Serial No.: 09/533,029

Filing Date: 22nd March, 2000

TECH CENTER 1600/2900

Examiner: Kruse, D.

Group Art Unit: 1638

Commissioner for Patents
Washington, D.C. 20231

DECLARATION UNDER 37 CFR 1.132 OF JACQUELINE E. HEARD

I, Jacqueline E. Heard, declare:

1. I received my doctoral degree from Boston College, Boston, Mass., in 1996. I have held the position of Senior Scientist at Mendel Biotechnology, Inc., Hayward, California, since March, 1998 and Director of the Genomics Program since January, 2002. In this declaration, I serve as an expert witness in that my work has involved the isolation and characterization of plant genes and the use of cloned genes to modify a variety of traits in genetically transformed plants, specifically in the areas of biotic and abiotic stress responses. I am also a named inventor of at least one of the non-selected sequences of the present application and I am therefore familiar with the instant invention.

2. This application relates to compositions and methods for modifying a plant's traits. The compositions include polynucleotides which encode novel plant transcription factor polypeptides first identified in *Arabidopsis thaliana*, a plant used experimentally as a model for all plant species. The methods include using the polynucleotides and polypeptides to modify a trait, such as a plant's response to environmental stress, in a transgenic plant.

3. I understand that the Examiner has rejected claims 17-36 directed to the described invention based on lack of enablement. The Examiner has stated that: 1) the specification does not provide reasonable enablement that a plant having the amino acid sequence of SEQ ID NO:18 can enhance the plant's tolerance to salt, heat, drought, osmotic stress, cold, freezing, or nutrient or pathogen stress 2) the specification does not provide reasonable enablement that a plant transformed with a polynucleotide encoding a polypeptide sequence of SEQ ID NO:18 can enhance the plant's tolerance to salt, heat, drought, osmotic stress, cold, freezing, or nutrient or pathogen stress, and 3) the specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

4. I would like to address the Examiner's concerns as to the enablement of the claimed invention by the specification. Applicants disclosed particular polynucleotide sequences encoding plant transcription factor polypeptides that were induced when plants were exposed to either biotrophic or necrotrophic plant pathogens, such as *Fusarium*, *Erysiphe*, and *Botrytis*; and disease associated growth-regulators such as methyl jasmonate (see specification at page 7, lines 22-27; page 8, lines 34-35; and page 19, lines 33-35). Applicants disclosed how to identify such induced polynucleotide sequences using RT-PCR and microarray experiments (see specification at page 19, lines 32-36; page 21, lines 10-28).

5. I herewith submit a set of four tables which report the results of such microarray analyses (Exhibits A-D). All these analyses were performed by one of the named inventors prior to the date of filing of the instant application. Exhibit A shows that mRNA levels of G28 (SEQ ID NO:17 of the instant application) was upregulated by at least 3-fold at 24 hours following treatment of native plants with the plant pathogen *Fusarium* (see Exhibit A, page 2). Exhibit B shows that mRNA levels of G28 (SEQ ID NO:17 of the instant application) was upregulated by at least 2.3-fold at 48 hours following treatment of native plants with *Fusarium* (see Exhibit B, page 11). Exhibit C shows that mRNA levels of G28 (SEQ ID NO:17 of the instant application) was upregulated by at least 2-fold at 7 days following treatment of native plants with the plant pathogen *Erysiphe* (see Exhibit C, page 19). Exhibit D shows that mRNA levels of G28 (SEQ ID NO:17 of the instant application) was upregulated by at least 2-fold at 24 hours following treatment of native plants with methyl jasmonate (see Exhibit D, page 3). In support of these results, a set of subsequent experiments, reported in Exhibits E, , shows that mRNA levels of G28 (SEQ ID NO:17 of the instant application) was upregulated by at least 2.6-fold at 12 hours following treatment of native plants with the plant pathogen *Botrytis* (see Exhibit E, page 4); was upregulated by at least . Applicants therefore had disclosed in the specification that they were in possession of the invention at the time the application was filed.

6. Applicants disclosed in the specification that the polynucleotides and polypeptides of the invention may be used to modify plant development, physiology or biochemistry such that the modified plants have a trait advantage over wild type plants (see specification at page 9, lines 21-23; page 16, lines 10-17; page 17, lines 10-15; page 21, line 32 through page 25, line 4).

7. I herewith submit a report of such analyses which show that when G28 (SEQ ID NO:17 of the instant application) is overexpressed in a transgenic plant, the transgenic plant is more resistant to infection with *Erysiphe*, as Applicants had predicted and disclosed in the specification (see Exhibit H, under heading "Mendel Discoveries").

8. In addition to the microarray analysis results for G28 (SEQ ID NO:17) as presented above, I would like to submit that mRNA levels of SEQ ID NO:12 (G4; Exhibit A, page 7), SEQ ID NO:22 (G19; Exhibit F, page 2), SEQ ID NO:34 (G1006; Exhibit A, page 2; Exhibit C, page 9; Exhibit E, page 4;

Exhibit F, page 1), and SEQ ID NO:82 (G25; exhibit G, page 4) also were upregulated by at least about 2-fold by plant pathogens such as *Fusarium*, *Erysiphe*, and *Botrytis*; and by methyl jasmonate, as Applicants disclosed in the Specification. Therefore, it is my contention that Applicants had disclosed several polynucleotide species in the instant application which, when overexpressed in a transgenic plant, would endow the plant with increased pathogen resistance.

9. It is my contention that one of ordinary skill in the art would have reasonably believed that Applicants therefore had disclosed the invention at the time the application was filed.

10. The function of SEQ ID NOs:17 and 18 (G28) has been analyzed using transgenic *Arabidopsis* plants in which this gene was expressed under the control of a 35S promoter, as disclosed in the specification. *Arabidopsis* plant lines overexpressing SEQ ID NO:17 (G28) repeatedly showed in laboratory experiments to be more tolerant to infections by *Erysiphe orontii*, *Sclerotinia sclerotiorum*, or *Botrytis cinerea*. In a repeat experiment using individual lines, all plant lines analyzed showed improved tolerance to *S. sclerotiorum* relative to control plants not transformed with the G28 transcription factor transgene (SEQ ID NO:17), and all but one of the lines tested were more tolerant to *B. cinerea* than controls.

11. The Examiner has asserted that Duggleby and Quattrocchio teach that the art of producing a desired phenotype by expression of a nucleic acid sequence encoding a heterologous transcription factor is unpredictable (Examiner's Office action, Paper No. 19, page 9).

It is my considered belief that one of ordinary skill in the art would consider that the teachings of Duggleby and Quattrocchio support the art of expressing a nucleic acid sequence in a transgenic plant to produce a desired phenotype is, in fact, predictable.

Duggleby teaches that one cannot predict the function of proteins encoded by DNAs sequences solely based on homology with another sequence, and that experiments are required in order to evaluate that function. However, Duggleby does not cite any relevant published work to substantiate his statement, and may have based his comment on his experience of enzymes, especially acetolactate synthases (ALS), not transcription factors, the matter of the instant invention claimed by Applicants.

The objective of the studies by Duggleby was to determine whether eukaryotic ALSs contain both small and large subunits, as earlier demonstrated in prokaryotic ALSs, and not only large subunits, as had been earlier suggested by protein purification studies of eukaryotic ALSs. The approach taken by Duggleby was to perform homology searches in GenBank to identify DNA sequences encoding eukaryotic versions of the small subunits. Duggleby teaches the identification of such sequences (Duggleby, Figure 2, page 247). Since experimental evidence of function was not presented in the paper, Duggleby prudently stated that the possibility existed that the algal and yeast sequences identified in GenBank may not encode functional ALS subunits. Duggleby also teaches that the studies so presented "may have significant practical implications" (Duggleby, page 248, column one, fourth paragraph, lines

7-8.)

The major assumption of the study, and the reason it was published in the first place, was that the eukaryotic (algal and yeast) sequences identified based on sequence homology were indeed, more likely than not, to encode small subunits of ALSs, a finding that had not been known earlier. This conclusion was confirmed by Duggleby in a later publication (Pang and Duggleby (1999) Biochemistry 38:5222-5231), which teaches that the yeast sequence described in the 1997 study is indeed the regulatory small subunit of acetolactate synthase.

To further support that the function of sequences identified by homology searches is predictable, Duggleby teaches that homology searches led to identification of some prokaryotic ALS small-subunits in earlier studies. (See Duggleby, page 245, introduction, paragraph bridging column one and two.) It is therefore my considered opinion that one of skill in the art would reasonably believe that the teachings of Duggleby do not present experimental evidence that weakens Applicants' claim that polynucleotides which encode polypeptide conserved domains with a high level of homology to Arabidopsis transcription factor conserved domains are likely to be transcription factors of similar function. In fact, Duggleby actually appears to rely on such an assumption in order to identify eukaryotic equivalents of prokaryotic enzymes (see Duggleby, page 248, section 3, note added in proof).

The Examiner has asserted that the teachings of Quattrocchio et al. (1998) demonstrate that one cannot extrapolate the effect of overexpressing a transcription factor from one plant species to another. It is my considered opinion that one of ordinary skill in the art would not interpret the teachings of Quattrocchio thus. Quattrocchio et al. teach that overexpression of specific petunia MYB and HLH genes induce anthocyanin production both in petunia and in corn. Reciprocally, the corn orthologues of the petunia genes produce the same effects in both species (see Quattrocchio, page 481, Figures 6j and 6k; and discussion on page 482, column one, third paragraph). Based on complementation analysis, Quattrocchio teaches that the transcription factors are interchangeable, in terms of the effect they have on anthocyanin accumulation. At the level of gene expression, Quattrocchio teaches that the maize and petunia transcription factors appear to have different effects on the very early genes in the pathway. However, Quattrocchio teaches that it is clearly demonstrable that the effect on the anthocyanin trait in maize of the petunia genes was predictable from overexpression data in petunia. Quattrocchio teaches that this is also true for the maize transcription factor.

Based on the teachings of Quattrocchio and others that describe the effect of Arabidopsis transcription factors in other species (as disclosed below in section 6), it is my considered opinion that one of skill in the art would reasonably believe that modulating expression of transcription factor genes is likely to affect the same trait in Arabidopsis as in other, even distantly related, plant species. It is therefore my considered opinion that one of skill in the art would reasonably believe that the data presented in the teachings of Duggleby and Quattrocchio are not inconsistent with Applicants' claims.

For example, Applicants did not rely exclusively on the annotation of the known database polynucleotide sequence hit; Applicants considered whether the claimed polynucleotides comprised conserved domains known in transcription factors; Applicants found that over-expression of the claimed

polynucleotides in a plant resulted in a modified trait, a characteristic of transcription factors well-known in the art.

It is my considered opinion that one of ordinary skill in the art would have a reasonable expectation that the analyses performed by Applicants and the disclosure by Applicants how to practice the invention is more reliable and more useful in describing how to use the invention than the teachings of Duggleby and Quattrocchio and that the teachings of Duggleby and Quattrocchio are not pertinent to refuting the instant invention.

12. I hereby declare that all statements made herein are true and that they are based on my own knowledge, information and belief. These statements are made with the knowledge that willful false statements are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of this application or any patent issued from it.

Date: 10/18/02

Jacqueline E. Heard
Jacqueline E. Heard, Ph.D.

EXHIBIT A

EID	COMMENT	(0.962)CY3CY5	(0.962)CY3METAROW	METACOL	ROW
E2228	3413711 (AC004747) putative antifungal protein [Arabid...	+3 285 17456.72	1280.88	3	3
E48	2642446 (AC002391) similar to auxin-responsive GH3 pro...	+2 39 8425.151	998.9	2	2
E840	4454029 (AL035394) tyrosine transaminase like protein ...	+3 396 2983.997	436.94	2	4
E132		1501.844	226.31	1	1
E1594	4559366 (AC006585) putative tyrosine transaminase [Ara...	+2 33 22878.68	3563.68	4	4
E741	3914996 PHOSPHOSERINE AMINOTRANSFERASE PRECURSO	26362.1	4325.66	2	3
E5728	2281111 (AC002333) endochitinase isolog [Arabidopsis t...	+2 990 3014.765	511.69	2	2
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th...	+2 564 6490.879	1134.63	4	3
E2202		6659.916	1285.26	1	3
E861	4220464 (AC006216) Similar to gb Y09437 myrosinase bin...	+1 4 7804.428	1520.45	2	2
E2230	1076442 beta-glucosidase (EC 3.2.1.21) - rape >emb CAA...	+2 4 15130.91	3007.93	3	3
E5447	4056465 (AC005990) F5O8.40 [Arabidopsis thaliana]	+3 396 6170.176	1277.74	3	3
E4332	G582	420.475	87.24	1	1
E1753	4388726 (AC006413) putative 12-oxophytodienoate-10,11-...	+1 5 4159.393	874.19	1	2
E3005	3548819 (AC005313) putative heterogeneous nuclear ribo...	+1 18 1562.678	336	1	2
E3703	2880054 (AC002340) putative cytochrome P450 [Arabidops...	+3 7 9131.384	2000.7	4	3
E1220	2894563 (AL021890) putative protein [Arabidopsis thali...	+1 293 5989.85	1318.85	1	3
E4349	G921	788.268	174.04	1	1
E5432	3193290 (AF069298) contains similarity to a protein ki...	+1 415 7 3363.522	760.18	1	1
E799	1703220 AIG2 PROTEIN >gil127806 (U40857) AIG2 [Arabid...	+1 9643.615	2197.57	2	2
E2339		835.638	192.31	1	2
E6736	3851530 (AF065435) nodulin [Glycine max]	+2 408 2.6 5522.092	1284.91	4	3
E489		8841.825	2072.92	1	1
E4131	A.thaliana cyclophilin	7934.189	1884.34	4	3
E2684		5655.337	1363.04	1	2
E3456	1755152 (U75187) germin-like protein [Arabidopsis thal...	+3 617 3673.234	888.09	4	3
E1458	1708924 MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (N	6396.602	1556.82	2	3
E5609	2129755 tryptophan synthase (EC 4.2.1.20) alpha chain ...	+1 561 1456.033	354.44	2	1
E772	2460188 (AF020785) polygalacturonase inhibiting protei...	+3 316 16190.16	4151.55	4	3
E618	1946365 (U93215) glutaredoxin isolog [Arabidopsis thal...	+2 504 5374.556	1413.26	3	2
E2084	4587610 (AC006951) putative indole-3-glycerol phosphat...	+2 413 15182.26	4017.26	4	4
E4218		3133.17	830.03	3	2
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th...	+2 564 6652.197	1766.4	2	2
E1704	3928099 (AC005770) unknown protein [Arabidopsis thaliana]	+2 3 2110.749	563.22	3	4

E4357	G921		941.849	254.08	3.707	3	1	20
E2367	312858 D-3-PHOSPHOGLYCERATE DEHYDROGENASE PREC		6289.9	1721.08	3.655	2	3	12
E6149	2832641 (AL021710) glycolate oxidase - like protein [A... +3 240		1566.672	428.89	3.653	1	1	4
E2503	510876 (X80051) NADP dependent malic enzyme [Phaseolu... +1		6325.547	1745.39	3.624	3	1	7
E5968	285286 flavonol 4'-sulfotransferase - Flaveria chlora... +2 218 3.4		2765.031	767.27	3.604	2	3	3
E6710			1372.362	381.28	3.599	2	1	5
E4590	G1535		420.244	121.82	3.45	2	4	19
E4844	G1006		820.278	237.88	3.448	1	2	21
E6757	3122858 D-3-PHOSPHOGLYCERATE DEHYDROGENASE PREC		3763.527	1099.37	3.423	4	3	5
E4463	G8		420.648	127.86	3.29	1	2	20
E3168	4468044 (X73587) catechol O-methyltransferase [Vanilla... +1 304		1776.11	541.33	3.281	3	3	14
E540	4587542 (AC006577) Belongs to the PF 00657 Lipase/Acyl... +3 3		5167.35	1578.21	3.274	1	1	9
E3011			479.884	146.78	3.269	3	2	14
E3857	3776578 (AC005388) ESTs gb F13915 and gb F13916 come f... +2		1282.04	394.52	3.25	1	3	16
E2546	3080393 (AL022603) NADH dehydrogenase like protein [Ar... +3 6		17691.61	5566.58	3.178	2	4	12
E3313	464367 POLYGALACTURONASE INHIBITOR PRECURSOR (PO 2137.109			676.39	3.16	1	4	14
E1758	2129600 glutathione synthase (EC 6.3.2.3) 2 - Arabidop... +2 441		2521.407	798.37	3.158	1	4	18
E2542	3434969 (AB008104) ethylene responsive element binding... +2 4		11704.1	3706.42	3.158	2	4	11
E4741	G759		1178.312	375.74	3.136	3	3	21
E5608	4581500 (AL034352) putative oxalyl-CoA decarboxylase [... +1 93		1903.34	610.41	3.118	2	1	2
E4461	G10		1015.848	329.02	3.087	1	4	20
E6869			2025.758	657.91	3.079	2	2	6
E5076	G28		2253.271	731.81	3.079	3	3	21
E822	2281113 (AC002333) endochitinase isolog [Arabidopsis t... +1 581		4007.227	1306.83	3.066	4	4	10
E2698	629602 probable imbibition protein - wild cabbage >em... +1 256		19582.08	6422.01	3.049	3	2	7
E1554	1170247 HEVEIN-LIKE PROTEIN PRECURSOR >gj 407248 (U018		2191.34	719.39	3.046	2	4	17
E1592			18700.53	6168.54	3.032	4	4	18
E28			16453.76	5428.88	3.031	4	2	7
E5067			1794.897	592.99	3.027	1	1	21
E2042			3832.55	1269.86	3.018	2	3	11
E4275	G198		491.01	162.96	3.013	1	2	22
E1312	3738340 (AC005170) GMP synthase-like protein [Arabidop... +2 4		1667.397	558.54	2.985	1	2	17
E4274			798.643	269.07	2.968	1	2	22
E2049	3851530 (AF065435) nodulin [Glycine max] +3 640 6.8		3177.951	1071.72	2.965	4	1	11
E6247			1701.813	579.35	2.937	1	4	4

E923	2801536 (AF039531) lysophospholipase homolog [Oryza sa...	+3	1163.116	469.13	2.479	1	1	11
E2578	4455220 (AL035440) putative aconitase [Arabidopsis tha...	+3	194 14524.35	5860.03	2.479	2	2	12
E2989			2371.224	960.68	2.468	1	2	13
E2449	3152575 (AC002986) Similar to cytochrome P450yr gb U3...	+2	1 472.426	191.95	2.461	1	1	7
E4638	G233		576.443	235.64	2.446	2	4	20
E4790	G881		611.782	251.02	2.437	1	4	20
E1613	4204303 (AC003027) lclprt_seq No definition line foun...	+1	576 5	247.18	2.425	1	1	18
E4540	G1356		492.492	203.27	2.423	2	1	20
E3325	G350		2639.764	1090.71	2.42	1	4	14
E3713	4105794 (AF049928) PGP224 [Petunia x hybrida]	+2	384	2063.86	2.408	4	1	16
E347	2244949 (Z97339) similarity to ORF - Lilium longifloru...	+2	659 1	207.65	2.407	2	1	8
E4206	G146		432.909	180.44	2.399	1	2	21
E5592			4330.778	1812.9	2.389	2	1	2
E6897			3872.076	1625.56	2.382	3	1	6
E4736	G839		1785.426	751.28	2.377	1	1	21
E2982	2584721 (Y10157) sulfite reductase [Arabidopsis thaliana]	+1	497	763.38	2.377	1	4	13
E5410	4220533 (AL035356) putative mitochondrial uncoupling p...	+1	938	187.63	2.373	1	1	3
E5814	2342686 (AC000106) Similar to Saccharomyces hypthetic...	+3	7 1499.467	634.29	2.364	3	3	3
E1657	4469019 (AL035602) putative protein [Arabidopsis thali...	+2	561	625.79	2.355	1	1	18
E6898	4468805 (AL035601) auxin-responsive GH3-like protein [...]	+1	693 2052.581	873.24	2.351	3	1	6
E5360	3128185 (AC004521) unknown protein [Arabidopsis thaliana]	+2	2	284.16	2.335	1	1	2
E317			856.628	367.33	2.332	4	1	8
E5399	2344900 (AC002388) EREBP isolog [Arabidopsis thaliana]	+3	5 7468.693	3214.26	2.324	3	3	2
E3204	3763924 (AC004450) putative extensin [Arabidopsis thal...	+3	270 2947.782	1271	2.319	3	3	14
E1756	2344900 (AC002388) EREBP isolog [Arabidopsis thaliana]	+1	8 865.376	373.32	2.318	1	4	18
E884			4327.564	1873.6	2.31	1	3	11
E5373	1169544 ERD1 PROTEIN PRECURSOR >pir JUN0901 ERD1 prote		9301.787	4030.96	2.308	3	3	2
E4050	pathogen-inducible protein CXc750		2339.339	1016.03	2.302	1	2	1
E2733			1195.655	521.19	2.294	1	3	13
E1265	1703220 AIG2 PROTEIN >gil 1127806 (U40857) AIG2 [Arabid...	+2	1503.076	655.28	2.294	1	1	17
E6567			418.387	182.93	2.287	1	1	5
E6413	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ		3563.077	1557.64	2.287	4	2	4
E4669	G564		1059.243	463.67	2.284	2	4	20
E3003	2642157 (AC003000) ankyrin-like protein [Arabidopsis t...	+1	125	399.63	2.277	1	2	14
E5248	2832641 (AL021710) glycolate oxidase - like protein [A...	+3	288	1005.32	2.275	4	2	7

E4005	3' flavonoid O-methyltransferase	2189.117	1012.27	2.163	2	3	1
E1612	1709498 OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >pir S	715.472	333.18	2.147	1	3	18
E6792	629602 probable imbibition protein - wild cabbage >em... +3 202	3928.242	1829.23	2.147	2	4	5
E4827	G186	884.605	412.81	2.143	1	2	21
E1493	2062164 (AC001645) jasmonate inducible protein isolog ... +1 555	8668.39	4044.58	2.143	2	1	18
E3396	3790567 (AF078821) RING-H2 finger protein RHA1b [Arabi... +2 6	1306.014	610.04	2.141	1	4	15
E2019		1806.561	844.14	2.14	2	1	11
E6890		498.805	233.21	2.139	1	1	6
E4899	G351	468.807	219.64	2.134	4	1	20
E694		2605.29	1221.45	2.133	2	1	10
E2183	2493391 PROBABLE STERIGMATOCYSTIN BIOSYNTHESIS P45	750.474	352.13	2.131	3	1	12
E5069	G189	1529.552	717.99	2.13	1	3	21
E6340		2848.664	1337.67	2.13	4	3	5
E6768		5407.104	2539.95	2.129	4	3	6
E1607	2660677 (AC002342) unknown protein [Arabidopsis thaliana] +2 6	1544.392	726.33	2.126	3	1	18
E6325	4337192 (AC006403) hypothetical protein [Arabidopsis t... +1 279	956.42	451.09	2.12	2	1	4
E2108	3549626 (AJ009696) wall-associated kinase 1 [Arabidops... +3 56	21140.26	10013.22	2.111	4	4	11
E2497		1091.08	518.8	2.103	1	1	7
E2690	3335363 (AC003028) hypothetical protein [Arabidopsis t... +1 414	3360.856	1601.09	2.099	3	2	7
E5742		558.282	266.08	2.098	1	1	3
E4745	G771	769.299	366.85	2.097	3	3	21
E3087	4263715 (AC006223) putative alanine acetyl transferase... +3 616	3258.543	1554.4	2.096	2	1	13
E3471	320556 chitinase (EC 3.2.1.14) precursor, basic - Ara... +2 630 5	15133.8	7230.46	2.093	4	1	14
E5942	3044214 (AF057044) acyl-CoA oxidase [Arabidopsis thali... +1 46	1872.495	895.61	2.091	2	3	3
E6199		1488.332	712.87	2.088	1	1	4
E6013		502.058	240.53	2.087	2	1	4
E6595	3399769 (U76299) uclacyanin II [Arabidopsis thaliana] +3 645	853.308	408.85	2.087	3	1	6
E3253	2252844 (AF013293) belongs to the cytochrome p450 fami... +3 5	5446.938	2611.25	2.086	2	2	18
E5132	G179	1570.31	755.61	2.078	1	3	21
E932	3115108 (AJ223983) plant uncoupling mitochondrial prot... +3 325	7786.864	3747.23	2.078	1	3	11
E2692	1708463 IAA-AMINO ACID HYDROLASE >gil887785 (U23794) l... 2825.989		1360.72	2.077	1	2	7
E5560		663.771	319.8	2.076	2	1	2
E3851	3894183 (AC005662) calmodulin-like protein [Arabidopsi... +3 462	5346.983	2578.95	2.073	3	3	16
E5714	3164138 (D78604) cytochrome p450 monooxygenase [Arabid... +2	1901.098	917.47	2.072	2	2	2
E4604	G452	1279.557	622.68	2.055	2	4	20

E2809	3668086 (AC004667) unknown protein [Arabidopsis thaliana] +2	1	7060.96	3450.37	2.046	1	1	13
E2768	4522009 (AC007069) unknown protein [Arabidopsis thaliana] +3	6	5992.959	2939.04	2.039	1	1	13
E4279			495.755	243.25	2.038	3	4	22
E1229			504.965	248.23	2.034	1	1	17
E1465			1214.883	597.15	2.034	2	1	17
E2141		1	3373.656	1658.36	2.034	2	2	11
E3077	2160189 (AC000132) Similar to A. thaliana receptor-lik...	2	1576.998	778.16	2.027	2	1	13
E2755			609.01	301.59	2.019	1	3	13
E6408	4587526 (AC007060) Strong similarity to F1913.2 glij303...	+1	255	3211.54	2.019	2	4	4
E5534	3702317 (AC005397) unknown protein [Arabidopsis thalia...	+3	35	1040.11	2.018	3	2	2
E3736	1695719 (D89342) luminal binding protein [Arabidopsis ...	+1	773	8566.57	2.017	4	3	15
E709			5121.048	2541.92	2.015	2	3	10
E1280	1171866 NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUN	2403.628		1194.5	2.012	1	3	17
E6319	1708971 (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSO	450.647		224.33	2.009	2	1	4
E2340	4249390 (AC005966) Similar to gblAF039182 probable ald...	+1	1	830.73	2.004	1	4	12
E5824	1617274 (Z72152) AMP-binding protein [Brassica napus]	+3	48	241.01	2.003	1	3	4
E1278			4257.732	2129.21	2	1	3	17
E5354	3935145 (AC005106) T25N20.9 [Arabidopsis thaliana]	+1	277	314.8	1.998	1	1	2
E5789	4585983 (AC005287) Unknown protein [Arabidopsis thaliana]	+3	3	504.9	1.997	1	1	4
E4324	G501		1115.573	558.87	1.996	3	1	19
E1491	3193289 (AF069298) similar to several small proteins (...	+1	415	718.43	1.994	2	1	18
E4460	G4		732.882	368	1.992	1	2	20
E1742	3080447 (AL022605) putative protein [Arabidopsis thali...	+1	250	211.04	1.99	1	4	18
E6291			878.455	441.74	1.989	3	4	4
E808	2832649 (AL021710) adenylosuccinate lyase - like prote...	+2	250	8782.61	1.989	4	4	10
E5681	2281111 (AC002333) endochitinase isolog [Arabidopsis t...	+2	775	921.58	1.988	4	2	2
E2627			8133.542	4097.73	1.985	4	4	12
E614			9547.846	4810.06	1.985	3	2	10
E6415	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ	5706.557		2880.97	1.981	4	4	4
E1166	1353163 HYPOTHETICAL 19.6 KD PROTEIN C23G10.2 IN CHRO	661.779		334.28	1.98	2	4	17
E6153	3892722 (AL033545) putative protein [Arabidopsis thali...	+1	262	294	1.979	1	1	4
E2154	3913518 3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-...	+3		568.98	1.974	2	4	11
E3393	2653885 (AF027408) phospholipase D-gamma; PLD-gamma [A...	+792.705		402.66	1.969	1	4	15
E968	585960 PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUN	1027.503		521.86	1.969	1	4	16
E2706			14849.41	7554.28	1.966	1	2	8

EXHIBIT B

EID	COMMENT	(0.845)CY%CY5	(0.845)CY%METAROV	METACOL	ROW
E2228	3413711 (AC004747) putative antifungal protein [Arabid... +3 285 2.8	26241.51	934.58	28.078	3
E48	2642446 (AC002391) similar to auxin-responsive GH3 pro... +2 390 4	22679.91	1008.78	22.483	2
E2067	417527 PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-	5345.965	245.81	21.748	2
E281	2746341 (AF037590) ATA27 [Arabidopsis thaliana] +3 330 1.2	20977.1	1046.73	20.041	3
E2692	1708463 IAA-AMINO ACID HYDROLASE >gj887785 (U23794) I... +1	8625.171	548.85	15.715	1
E840	4454029 (AL035394) tyrosine transaminase like protein ... +3 396 4.8	5600.37	362.92	15.431	2
E3855	4099847 (U90523) saccharopine dehydrogenase [Arabidops... +3 655	4998.476	348.2	14.355	1
E5728	2281111 (AC002333) endochitinase isolog [Arabidopsis t... +2 990 5.	3633.133	264.47	13.737	2
E2632		13960.51	1089.66	12.812	1
E2339		1874.27	155.97	12.017	1
E3471	320556 chitinase (EC 3.2.1.14) precursor, basic - Ara... +2 630 5.2e	27910.36	2555.41	10.922	4
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	3636.445	345.23	10.533	1
E3884	480907 peroxidase (EC 1.11.1.7) - Arabidopsis thalian... +3 493 2.6e	4940.54	471.71	10.474	3
E4579	G1329	565.646	60.68	9.322	2
E6646	3164144 (D78607) cytochrome P450 monooxygenase [Arabid... +1 3	1978.575	227.02	8.715	1
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	1832.329	213.28	8.591	2
E6757	3122858 D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECUR	6416.669	753.41	8.517	4
E2202		6417.184	761.45	8.428	1
E337	1064887 (X92955) pollen coat protein [Brassica oleracea] +3 287 1.1	2070.147	253.51	8.166	2
E2230	1076442 beta-glucosidase (EC 3.2.1.21) - rape >emb CAA... +2 428	29303.86	3656.44	8.014	3
E6710		1625.231	202.96	8.008	2
E4741	G759	1367.624	182.43	7.497	3
E4540	G1356	997.889	140.27	7.114	2
E5609	2129755 tryptophan synthase (EC 4.2.1.20) alpha chain ... +1 561 8.1	1437.026	209.08	6.873	2
E2493		5311.873	779.18	6.817	1
E132		2126.005	326.34	6.515	1
E1909		4038.617	634.67	6.363	1
E2367	3122858 D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECUR	6550.174	1040.77	6.294	2
E5432	3193290 (AF069298) contains similarity to a protein ki... +1 415 7.0e	2909.183	464.07	6.269	1
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	1357.147	220.68	6.15	2
E508		10058.84	1642.78	6.123	3
E822	2281113 (AC002333) endochitinase isolog [Arabidopsis t... +1 581 2.	6187.663	1024.78	6.038	4
E6869		2052.945	350.49	5.857	2
E5145		1076.213	185.61	5.798	1
E4522		1160.848	201.3	5.767	4
E4064	cinnamyl alcohol dehydrogenase	6404.071	1115.55	5.741	3

E2044	G413		8215.125	1439.94	5.705	2	3	11
E4064	cinnamyl alcohol dehydrogenase		9413.741	1680.23	5.603	4	2	1
E489			12511.85	2240.82	5.584	1	1	9
E4056	PUTATIVE TRYPSIN INHIBITOR T01024.25 PRECURSOR		5214.361	934.57	5.579	1	2	1
E799	1703220 AIG2 PROTEIN >gj1127806 (U40857) AIG2 [Arabid... +1 1(10606.56	1919.37	5.526	2	2	10
E540	4587542 (AC006577) Belongs to the PF100657 Lipase/Acyl... +3 372		5381.908	983.37	5.473	1	1	9
E1753	4388726 (AC006413) putative 12-oxophytodienoate-10,11-... +1 528		4492.811	838.27	5.36	1	2	18
E4443	G413		781.235	147.46	5.298	1	2	19
E1025	2347199 (AC002338) protein kinase isolog [Arabidopsis ... +3 464 3.(1605.578	311.18	5.16	1	2	16
E741	3914996 PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (I		27153.38	5269.4	5.153	2	3	10
E2353	2708482 (U79556) IAA25 [Arabidopsis thaliana] +3 524 1.3e-		2395.347	472.78	5.067	1	2	12
E5688	2829900 (AC002311) similar to ripening-induced protein... +3 610 1.7		1591.958	319.97	4.975	2	2	2
E1107			10905.2	2199.04	4.959	4	1	16
E861	4220464 (AC006216) Similar to gb Y09437 myrosinase bin... +1 438		8106.207	1674.02	4.842	2	2	10
E4064	cinnamyl alcohol dehydrogenase		3202.048	672.23	4.763	3	2	1
E1704	3928099 (AC005770) unknown protein [Arabidopsis thaliana] +2 380		3115.934	659.56	4.724	3	4	18
E1783	4589123 (AF126374) At14a protein [Arabidopsis thaliana] +1 566 4.		5073.818	1077.72	4.708	3	2	19
E772	2460188 (AF020785) polygalacturonase inhibiting protei... +3 316 7.7		9696.348	2067.18	4.691	4	3	10
E2305			4939.265	1054.72	4.683	1	2	12
E1114	G1745		11382.47	2462.16	4.623	2	3	16
E1612	1709498 OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >pir S57..		922.894	200.04	4.614	1	3	18
E4143	A.thaliana beta tubulin 1		1241.157	269.19	4.611	2	3	22
E1312	3738340 (AC005170) GMP synthase-like protein [Arabidop... +2 472		2114.581	463.92	4.558	1	2	17
E725	G242		8600.677	1894.92	4.539	4	3	10
E3566	417381 NITRILASE 1 >pir S22398 nitrilase (EC 3.5.5.1... +2 530 3.1		4137.396	919.32	4.5	1	1	15
E2698	629602 probable imbibition protein - wild cabbage >em... +1 256 4.2		24401.53	5473.63	4.458	3	2	7
E6637	584825 B2 PROTEIN >pir S32124 B2 protein - carrot >e... +3 698 9		7016.585	1591.59	4.409	3	2	5
E4064	cinnamyl alcohol dehydrogenase		6661.746	1512.23	4.405	4	1	1
E2183	2493391 PROBABLE STERIGMATOCYSTIN BIOSYNTHESIS P450 M		2111.033	480.57	4.393	3	1	12
E4617	G610		3202.226	730.62	4.383	4	2	20
E1962			2674.668	615.73	4.344	1	4	11
E4745	G771		811.272	187.36	4.33	3	3	21
E3857	3776578 (AC005388) ESTs gb F13915 and gb F13916 come f... +2 1:		1101.239	254.36	4.329	1	3	16
E2684			4195.941	974.06	4.308	1	2	7
E3703	2880054 (AC002340) putative cytochrome P450 [Arabidops... +3 745		11312.49	2645.42	4.276	4	3	15
E3168	4468044 (X73587) catechol O-methyltransferase [Vanilla... +1 304 2.		1168.41	274.18	4.261	3	3	14
E1465			3545.727	834.59	4.248	2	1	17

E1423	1944132 (AB002560) CUC2 [Arabidopsis thaliana]	+3 491 4.2	8204.91	1935.13	4.24	4	1	17
E6149	2832641 (AL021710) glycolate oxidase - like protein [A...	+3 240 2.1e	1413.546	334.64	4.224	1	1	4
E2065	3810848 (AL032684) putative autophagy protein [Schizos...	+1 214 9	2975.391	704.65	4.223	2	1	11
E775	4432837 (AC006283) hypothetical protein [Arabidopsis t...	+3 314 2.4	12648.89	2998.73	4.218	2	2	9
E329	4262182 (AC005508) 44123 [Arabidopsis thaliana]	+1 426 6.6e	10566.64	2513.16	4.205	4	1	9
E2291	4432835 (AC006283) unknown protein [Arabidopsis thaliana]	+1 155	3683.769	876.61	4.202	3	2	12
E5714	3164138 (D78604) cytochrome p450 monooxygenase [Arabid...	+2 7e	2166.02	519.27	4.171	2	2	2
E1654	1762933 (U66263) tumor-related protein [Nicotiana taba...	+3 178 1.5	5462.564	1313.58	4.159	3	3	18
E2740			837.904	202.35	4.141	1	1	13
E6138			2656.097	645.54	4.115	1	1	4
E1431	2342687 (AC000106) Similar to Beta integral membrane p...	+3 510 4	7026.91	1745.58	4.026	2	1	17
E5447	4056465 (AC005990) F5O8.40 [Arabidopsis thaliana]	+3 396 2.1	3186.037	806.14	3.952	3	3	3
E4827	G186		1267.586	321.09	3.948	1	2	21
E6759	2827709 (AL021684) predicted protein [Arabidopsis thal...	+1 272 2.1	1520.96	387.9	3.921	2	1	6
E1594	4559366 (AC006585) putative tyrosine transaminase [Ara...	+2 335 2	24135.77	6211.36	3.886	4	4	18
E4337	G736		328.368	85.04	3.861	1	1	20
E2084	4587610 (AC006951) putative indole-3-glycerol phosphat...	+2 413 5	12802.09	3320.21	3.856	4	4	10
E2628	1946364 (U93215) lipase isolog [Arabidopsis thaliana]	+2 391 6.0e	17847.47	4648.96	3.839	4	2	12
E6708			7229.817	1885.83	3.834	4	1	5
E5229	3759184 (AB018441) phi-1 [Nicotiana tabacum]	+3 182 2.0e	4490.149	1172.17	3.831	2	2	7
E2678	1181531 (L41244) thionin [Arabidopsis thaliana] >prfll...	+2 430 7.9e	3621.575	947.61	3.822	3	2	8
E2153			3142.862	823.5	3.816	2	2	11
E1093	2194118 (AC002062) F20P5.4 gene product [Arabidopsis t...	+1 326	9798.499	2574.63	3.806	2	1	17
E6975	4262181 (AC005508) 37496 [Arabidopsis thaliana]	+2 694 2.4e	940.646	248.38	3.787	1	1	7
E4145	A.thaliana beta tubulin 1		841.419	222.3	3.785	2	3	22
E6898	4468805 (AL035601) auxin-responsive GH3-like protein [...]	+1 693 1	2677.938	708.59	3.779	3	1	6
E4505	G773		710.051	188.39	3.769	4	3	19
E4265	G255		2151.454	572.93	3.755	3	4	22
E5529	2583108 (AC002387) putative surface protein [Arabidops...	+1 602 1	4747.747	1268.47	3.743	1	4	2
E5592			3942.821	1058.63	3.724	2	1	2
E1950	1491776 (M37636) cationic peroxidase [Arachis hypogaea]	+2 403 3	526.113	141.62	3.715	1	4	11
E4026	thionin		621.816	167.38	3.715	1	1	1
E4687	G663		2720.868	733.34	3.71	1	1	20
E4131	A.thaliana cyclophilin		2035.751	549.07	3.708	4	3	22
E6340			3050.073	824.03	3.701	4	3	5
E5681	2281111 (AC002333) endochitinase isolog [Arabidopsis t...	+2 775 3	2258.724	613.68	3.681	4	2	2
E5544	2190555 (AC001229) No definition line found [Arabidops...	+2 252 1	4114.71	1119.47	3.676	1	2	2

E6581	4337027 (AF123254) MFP2 [Arabidopsis thaliana]	+1 207 6.9e	1511.767	411.75	3.672	1	1	6
E1451	2911039 (AL021961) cinnamyl alcohol dehydrogenase - li...	+3 513 6	9788.639	2674.95	3.659	4	1	18
E5493	2065013 (Y11650) cyclic phosphodiesterase [Arabidopsis...	+2 796 4	4214.216	1156.65	3.643	3	2	2
E1056	4559358 (AC006585) putative steroid binding protein [A...	+3 203 1.4	2258.124	624.94	3.613	3	4	17
E5365			10975.95	3048.66	3.6	3	3	2
E6471	1009712 (U27698) calreticulin [Arabidopsis thaliana]	+2 611 8.0e-	5768.686	1606.91	3.59	2	2	4
E884	G681		6483.037	1807.27	3.587	1	3	11
E4728			673.711	187.99	3.584	3	1	21
E3308	849074 (D50737) B-type cyclin [Nicotiana tabacum]	+1 126 9.2e	728.766	204.38	3.566	1	2	14
E3736	1695719 (D89342) luminal binding protein [Arabidopsis ...	+1 773 5.4	15678.82	4406.35	3.558	4	3	15
E4432	G562		1011.551	284.65	3.554	1	2	19
E5593	4309731 (AC006439) hypothetical protein [Arabidopsis t...	+2 216 6.0	1237.659	349.21	3.544	2	1	2
E5623			5061.279	1428.23	3.544	4	3	2
E6768			10466.59	2960.92	3.535	4	3	6
E3069			4674.975	1328.62	3.519	4	1	13
E1865	3367517 (AC004392) Similar to F4I1.26 putative beta-gl...	+2 697 6.1	8544.482	2440.28	3.501	2	1	19
E6635	2829898 (AC002311) Hypothetical protein [Arabidopsis t...	+2 594 5.	1129.679	327.36	3.451	1	4	5
E2500	1362106 GUT 7-2a protein - common tobacco (fragment)	+3 283	14067.35	4090.82	3.439	3	3	7
E586	2598597 (Y15371) MtN5 [Medicago truncatula]	+2 181 3.0e-	2695.157	785.17	3.433	1	2	9
E6342	3319340 (AF077407) contains similarity to E. coli cati...	+1 187 5.9e-	6024.019	1767.63	3.408	2	1	4
E1657	4469019 (AL035602) putative protein [Arabidopsis thali...	+2 561 1.6e	2096.433	616.22	3.402	1	1	18
E4242	G358		1044.638	307.39	3.398	1	2	21
E179	4662633 (AC007267) hypothetical protein [Arabidopsis t...	+3 263 6.0	2088.702	615.2	3.395	1	3	9
E4591	G263		2472.809	734.44	3.367	4	2	19
E4270			1059.72	315.64	3.357	1	2	22
E5248	2832641 (AL021710) glycolate oxidase - like protein [A...	+3 288 1.4e	3378.416	1007.68	3.353	4	2	7
E3859			2080.835	620.94	3.351	1	3	16
E1374	4725948 (AL049730) putative Phospholipase D [Arabidops...	+3 382	1474.025	441.26	3.34	1	4	17
E932	3115108 (AJ223983) plant uncoupling mitochondrial prot...	+3 325 1.	7638.748	2304.71	3.314	1	3	11
E3559	3063472 (AC003981) F22O13.34 [Arabidopsis thaliana]	+1 669 6	7706.46	2341.79	3.291	1	3	16
E2323			4204.584	1286.29	3.269	3	2	12
E5640	2827524 (AL021633) predicted protein [Arabidopsis thal...	+2 100 3.3	1429.236	439.1	3.255	2	1	2
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th...	+2 564 7.1	8524.863	2620.78	3.253	4	3	7
E4945	G39		535.39	165.5	3.235	4	1	20
E5468	4512701 (AC006569) putative tyrosine decarboxylase [Ar...	+2 538 4.	2674.263	827.9	3.23	1	2	2
E6918	2493289 RIBONUCLEASE 1	+3 94 2.3e-08	2612.44	811.19	3.221	1	1	7
E2788	1523796 (X97864) cytochrome P450 [Arabidopsis thaliana]	+1 296	463.589	144.08	3.218	1	1	13

E1525	2160152 (AC000375) ESTs gb U75592.gb T13956.gb T43869 ... +2 4	1193.952	372.08	2	2	17
E986	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ23.	1642.873	514.32	3	2	16
E2513	1170121 GLUTATHIONE S-TRANSFERASE 103-1A >pir S66354 ... +	9025.839	2829.33	3	1	8
E6297	584825 B2 PROTEIN >pir S32124 B2 protein - carrot >e... +2 240 1	10103.31	3167.04	1	2	5
E2340	4249390 (AC005966) Similar to gb AF039182 probable ald... +1 178	2099.542	659.45	1	4	12
E2733		1145.47	359.92	1	3	13
E417	4406765 (AC006836) putative cold-regulated protein cor... +3 458 1.5	569.71	179.07	2	2	9
E1935	4210330 (AJ223802) 2-oxoglutarate dehydrogenase, E1 su... +2 408	3925.086	1233.81	1	2	11
E1554	1170247 HEVEIN-LIKE PROTEIN PRECURSOR >gi 407248 (U018... +	2130.305	670.85	2	4	17
E6133		1012.557	320.47	1	1	4
E3834	729470 MITOCHONDRIAL FORMATE DEHYDROGENASE PRECUR	7973.141	2527.07	2	2	16
E5223	1403134 (X98453) peroxidase [Arabidopsis thaliana] +3 485 1.8	2195.854	697.49	4	4	6
E657	629670 hypothetical protein - tomato +2 422 8.5e-39 1	2718.638	863.72	1	4	10
E4431	G515	881.493	280.69	1	2	19
E2137	3164222 (AB008518) RMA1 [Arabidopsis thaliana] >gi 420... +1 413	5228.243	1669.59	2	2	11
E971		3192.568	1027.78	1	2	16
E6211	G242	1413.013	456.77	3	1	5
E5773	3894194 (AC005662) putative strictosidine synthase [Ar... +2 742 1.1	934.706	302.29	1	1	3
E242	4454461 (AC006234) putative cell wall protein precursor... +2 593 6.5	629.074	204.02	1	2	9
E516	2281627 (AF003094) AP2 domain containing protein RAP2... +2 764	7886.444	2561.22	1	3	10
E5325	3859607 (AF104919) contains similarity to cysteine pro... +3 329 6.3	1888.651	614.07	2	1	7
E3553	4544458 (AC006592) unknown protein [Arabidopsis thaliana] -1 593	1296.989	422.39	1	1	15
E6743	3540182 (AC004122) Unknown protein [Arabidopsis thaliana] +3 823	1027.638	336.24	2	1	5
E514	2462824 (AF000657) similar to Jun activation domain bi... +2 740 2.4	2946.841	964.35	1	3	10
E6413	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ23.	3491.441	1144.13	4	2	4
E1013		1858.2	611.58	1	2	16
E2578	4455220 (AL035440) putative aconitase [Arabidopsis tha... +3 194 2.	11752.62	3887.31	2	2	12
E5434	3334124 ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECU	926.789	306.78	1	1	2
E6013		632.986	209.73	2	1	4
E2056	1168257 ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC ISOZ	2558.915	849.02	2	3	11
E5984	3236255 (AC004684) hypothetical protein [Arabidopsis t... +2 115 3.5	2894.085	962.16	2	3	4
E1278		4515.97	1503.75	1	3	17
E6110	4115383 (AC005967) receptor-like protein kinase [Arabi... +1 608 1.7	999.258	334.01	2	2	4
E6649	544256 ESTERASE FE4 PRECURSOR (CARBOXYLIC-ESTER HYDI	1772.644	593.07	1	2	6
E3753	2062156 (AC001645) jasmonate inducible protein isolog ... +2 580 1.	2890.485	967.72	2	2	15
E6409		3534.836	1186.38	2	2	4
E2211	3281848 (AL031004) putative protein [Arabidopsis thali... +3 185 1.2	1005.594	338.26	1	1	12

EXHIBIT C

EID	COMMENT	(1.243)CY3	CY5	CY5/(1.243)CY3	SOURCE
E2067	417527 PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR	827.813	37800.35	45.663	L20P15F02,L35P91G09
E822	2281113 (AC002333) endochitinase isolog [Arabidopsis t... +1	316.816	10493.82	33.123	L18P29E04,L35P88H06
E3713	4105794 (AF049928) PGP224 [Petunia x hybrida](germinating i	613.619	15984.65	26.05	L17P17D04,L35P107H01
E2050		1354.82	30604.31	22.589	L20P13A01,L35P91D10
E3171	481821 probable glutathione transferase (EC 2.5.1.18)... +3	1805.183	32667.3	18.096	L15P4C09,L35P101E03
E5077	G354	260.781	3452.33	13.238	J129B10F1
E1197		409.892	5347.98	13.047	L18P10G01,L35P112F07
E5291		236.307	2837.19	12.006	J56A10F1
E2788	1523796 (X97864) cytochrome P450 [Arabidopsis thaliana] +1	817.956	9539.21	11.662	L23P5G04,L35P97C07
E4570	G1043	688.51	8022.4	11.652	J123D08F1
E1106	2129634 lectin-like protein - Arabidopsis thaliana >em... +1	1484.154	14031.72	9.454	L17P3E09,L35P111B08
E4564	G920	554.987	5000.25	9.01	J123C06F1
E2084	4587610 (AC006951) putative indole-3-glycerol phosphat... +2	1567.895	14004.82	8.932	L20P17H02,L35P92B02
E501	4115383 (AC005967) receptor-like protein kinase [Arabi... +1	1215.952	10226.37	8.41	L17P32C01,L35P85C01
E2108	3549626 (AJ009696) wall-associated kinase 1 [Arabidops... +3	3415.427	28051.43	8.213	L20P2G11,L35P92F02
E1374	4725948 (AL049730) putative Phospholipase D [Arabidops... +3	211.459	1685.88	7.973	L18P33H09,L35P114C12
E2049	3851530 (AF065435) nodulin [Glycine max] +3	1105.126	8567.78	7.753	L20P12H08,L35P91D09
E1491	3193289 (AF069298) similar to several small proteins (... +1	1014.039	7710.42	7.604	L20P16E07,L35P115G09
E3173	3241945 (AC004625) unknown protein [Arabidopsis thaliana] +2	1080.999	8143.19	7.533	L15P4D01,L35P101E05
E2737	4115914 (AF118222) contains similarity to Iron/Ascorba... (oxidic	1083.299	8023.51	7.407	L23P2E08,L35P97B04
E1220	2894563 (AL021890) putative protein [Arabidopsis thali... +1	498.182	3485.66	6.997	L18P1D03,L35P113A06
E764	3608142 (AC005314) putative hin1 [Arabidopsis thaliana] +1	1277.244	8309.28	6.506	L18P15H06,L35P87G08
E250	2618727 (U49075) IAA19 [Arabidopsis thaliana] +2	906.955	5856.28	6.457	L17P17D08,L35P82A07
E4450	G354	141.217	906.06	6.416	J122C12F1
E1466	3883128 (AF082302) arabinogalactan-protein [Arabidopsi... +2	333.186	2121.66	6.368	L20P10A05,L35P115C08
E2109	2052383 (U66345) calreticulin [Arabidopsis thaliana] +1	3952.602	25069.4	6.343	L20P2H03,L35P92F03
E1080		1031.615	6493.24	6.294	L17P41F08,L35P111D04
E3748	4324714 (AF110771) ammonium transporter [Arabidopsis t... +1	3181.631	19053.99	5.989	L17P17F09,L35P107H08
E4790	G881	163.703	973.87	5.949	J126C04F1
E1909		2874.859	17006.95	5.916	L18P5C02,L35P90E01
E6546		299.227	1768.78	5.911	J44B06F1
E4591	G263	404.82	2350.01	5.805	J124B01F1
E2211	3281848 (AL031004) putative protein [Arabidopsis thali... +3	1047.028	6060.78	5.789	L22P12B01,L35P93G03
E2533		301.925	1743.19	5.774	L15P7B11,L35P77G11
E4737	G271	1043.56	6016.65	5.766	J125G04F1
E1460	3451056 (AL031326) serine/threonine kinase - like prot... +1	1022.641	5735.08	5.608	L18P8F11,L35P115B08

E3736	1695719 (D89342) luminal binding protein [Arabidopsis ... +1 77	2829.067	15827.06	5.594	L17P16D02,L35P107D08
E3703	2880054 (AC002340) putative cytochrome P450 [Arabidops... +3	1164.715	6491.31	5.573	L17P16C08,L35P107D06
E1843		841.946	4669.77	5.546	L24P12H04,L35P119B07
E1465		895.519	4883.32	5.453	L20P10A03,L35P115C07
E4418	G1417	105.469	573.32	5.436	J122F04F1
E1807	4741198 (AL049746) putative protein [Arabidopsis thali... +2 46	790.498	4187.03	5.297	L24P5F09,L35P119D01
E2086		2232.315	11762.04	5.269	L20P1A01,L35P92B04
E1867	2435406 (U83490) thaumatin-like protein [Arabidopsis t... +2 57	708.721	3730.18	5.263	L28P1F06,L35P119F07
E2059	2924777 (AC002334) putative receptor protein kinase [A... +2 1	972.287	5061.03	5.205	L20P14E08,L35P91F07
E586	2598597 (Y15371) MtN5 (nodulin) [Medicago truncatula]	1540.599	8007.6	5.198	L17P3F04,L35P86A03
E2968		1552.158	8058.3	5.192	L24P5H11,L35P98A10
E2056	1168257 ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC	1221.11	6300.68	5.16	L20P14B07,L35P91E10
E3226	4262180 (AC005508) 29621 [Arabidopsis thaliana] +2 62	2620.79	13519.8	5.159	L15P4F04,L35P101F10
E3478	322551 nucleoside-diphosphate kinase (EC 2.7.4.6) - A... +1 4	2990.607	15420.6	5.156	L16P10C07,L35P103E12
E4761	G1048	602.668	3045.46	5.053	J125D07F1
E3848		989.055	4966.92	5.022	L17P21F07,L35P109B01
E1454	3688186 (AL031804) putative protein [Arabidopsis thali... +3 67	1204.616	5951.48	4.941	L18P6F12,L35P115A08
E3851	3894183 (AC005662) calmodulin-like protein [Arabidopsi... +3 4	717.646	3514.61	4.897	L17P21G01,L35P109B04
E5067		422.868	2066.26	4.886	J129A09F1
E2551		1396.199	6808.46	4.876	L22P8E01,L35P96B05
E4827	G186	167.196	813.94	4.868	J126C05F1
E2724	1174498 SYNAPTOBREVIN-RELATED PROTEIN >gj600710 (A	2295.584	11050.18	4.814	L16P1A07,L35P78H09
E4329	G536	847.49	4048.24	4.777	J121D11F1
E2807		729.902	3457.74	4.737	L24P12H08,L35P97F11
E4356	G993	660.555	3107.25	4.704	J121H01F1
E567		1882.97	8834.27	4.692	L17P37H03,L35P85F08
E2111	2739381 (AC002505) putative patatin (storage protein) [Arabid	3224.552	15064.2	4.672	L20P2H07,L35P92F05
E1011	4263818 (AC006067) unknown protein [Arabidopsis thaliana] +3	969.254	4524.51	4.668	L17P37F07,L35P110H04
E4918	G348	224.958	1048.51	4.661	J127F10F1
E1704	3928099 (AC005770) unknown protein [Arabidopsis thaliana] +2	1303.496	6015.49	4.615	L22P7D12,L35P118B06
E4108	GP-39	281.738	1293.53	4.591	O17202,M80927
E2256		1313.117	5988.01	4.56	L22P11F05,L35P93F12
E4324	G501	559.138	2527.11	4.52	J121D01F1
E5069	G189	407.269	1839.87	4.518	J129A10F1
E3683	1170505 EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >	967.377	4351.28	4.498	L17P13G06,L35P107A02
E3884	480907 peroxidase (EC 1.11.1.7) - Arabidopsis thalian... +3 49	1570.12	7037.43	4.482	L17P27B07,L35P109H01
E3728	4490728 (AL035709) putative protein [Arabidopsis thali... +1 51	1568.864	7000.53	4.462	L17P15D09,L35P107B11

E1455	128188 NITRATE REDUCTASE 2 (NR2) >pir RDMUNH nitrate .	2636.937	11752.94	4.457	L18P6G08,L35P115A09
E4345	G867	1878.881	8286.92	4.411	J121F11F1
E6768		1191.937	5161.98	4.331	J46F06F1
E4051	NITRATE REDUCTASE 2	1006.867	4332.01	4.302	L18P6G08F1
E3476		846.172	3610.37	4.267	L16P10C02,L35P103E10
E1714		889.689	3792.26	4.262	L22P9A11,L35P118D04
E1450	2914705 (AC003974) putative disease resistance protein... +1 2	436.392	1851.87	4.244	L20P17C01,L35P115H04
E3704	625977 (ribosome associated) p40 protein homolog - Arabidop	2388.536	10120.36	4.237	L17P16D11,L35P107E01
E1962		2509.318	10594.89	4.222	L18P5H12,L35P90E12
E4349	G921	644.035	2699.53	4.192	J121G09F1
E4514	G986	121.466	501.9	4.132	J123C12F1
E3578	4406816 (AC006201) 60S ribosomal protein L2 [Arabidops... +1	2857.905	11804.49	4.13	L16P5H09,L35P105G07
E2914		1163.037	4784.6	4.114	L16P5H12,L35P79H10
E4051	NITRATE REDUCTASE 2	1845.842	7556.55	4.094	L18P6G08F1
E3430	3687251 (AC005169) unknown protein [Arabidopsis thaliana] +1	672.811	2726.26	4.052	L16P10A11,L35P103E06
E3698	4582468 (AC007071) putative 40S ribosomal protein; con... +1	1421.308	5750.34	4.046	L17P15G01,L35P107C05
E3711	4506685 ribosomal protein S13 >sp Q02546 RS13_HUMAN 40..	1670.517	6739.3	4.034	L17P17B02,L35P107G02
E3727	3036808 (AL022373) DnaJ-like protein [Arabidopsis thal... +2 5i	3228.231	12983.32	4.022	L17P15D06,L35P107B10
E3422	1350707 60S RIBOSOMAL PROTEIN L29 >pir JC2012 ribosom	1136.164	4557.43	4.011	L15P9F02,L35P103D04
E5011		214.007	855.56	3.998	J128B05F1
E2382	2213626 (AC000103) F21J9.18 [Arabidopsis thaliana] +2 4	966.01	3846.92	3.982	L22P3G11,L35P95E05
E2367	3122858 D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRE	3569.062	14193.76	3.977	L22P2A02,L35P95C02
E2684		1927.656	7643.96	3.965	L15P8B11,L35P78A11
E1287	G742	1943.169	7689.49	3.957	L18P28C09,L35P113E07
E4051	NITRATE REDUCTASE 2	945.587	3738.56	3.954	L18P6G08F1
E3225	730526 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOI	2407.752	9514.55	3.952	L15P4F03,L35P101F09
E2759	G415	489.008	1909.65	3.905	L24P10G03,L35P97F02
E3699	2576363 (U39783) amino acid transport protein [Arabido... +3 5	311.11	1212.88	3.899	L17P15G07,L35P107C06
E3447	3123279 40S RIBOSOMAL PROTEIN S26 >gi 2651298 (AC002	1007.948	3920.42	3.89	L16P11D03,L35P103H05
E2857	4455210 (AL035440) putative aspartate-tRNA ligase [Ara... +3 2	1187.052	4605.89	3.88	L16P5D02,L35P79G01
E1525	2160152 (AC000375) ESTs gb U75592.gb T13956.gb T43869 ...	403.154	1561.66	3.874	L20P7B02,L35P116E01
E2771	1703227 ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC	2775.904	10751.83	3.873	L24P2D05,L35P97H02
E4069	caffeic o-methyltransferase	472.974	1826.18	3.861	L34P4G06F1
E4039	HIGH AFFINITY AMMONIUM TRANSPORTER	1654.109	6386.55	3.861	L17P17F09F1
E3187	1710780 40S RIBOSOMAL PROTEIN S9 (S7) >emb CAA65433	2046.537	7871.84	3.846	L15P4H08,L35P101H01
E2774	3021269 (AL022347) putative protein [Arabidopsis thali... +1 41	2969.688	11418.22	3.845	L24P2E06,L35P97H05
E3901	4512675 (AC006931) putative citrate synthase [Arabidop... +2 5	1053.131	4012.78	3.81	L17P22B10,L35P109B12

E4912	G1113		365.566	1389.8	3.802	J127E11F1
E741	3914996	PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR	766.632	2902.38	3.786	L17P9G05,L35P87C08
E1652	4206789	(AF112864) syntaxin-related protein At-SYR1 [A... +2]	1022.69	3844.4	3.759	L22P13F02,L35P117B08
E5132	G179		124.213	466.82	3.758	J129A08F1
E3729	3702339	(AC005397) unknown protein [Arabidopsis thaliana] +2	2351.432	8791.02	3.739	L17P15E02,L35P107B12
E1688	4490297	(AL035678) putative protein [Arabidopsis thaliana] +1	951.355	3545.15	3.726	L22P2B03,L35P117H08
E3801	1619300	(X95269) LRR protein [Lycopersicon esculentum] +2	4021.352	14933.01	3.713	L17P18C12,L35P108A10
E670	3548818	(AC005313) unknown protein [Arabidopsis thaliana] +2	1222.664	4531.19	3.706	L17P7B05,L35P86G09
E3247	2369714	(Z97178) elongation factor 2 [Beta vulgaris] +1	5192.854	19190.04	3.695	L33P7H04,L35P120B01
E2990			1304.777	4814.44	3.69	L28P3C02,L35P98E08
E4039	HIGH AFFINITY AMMONIUM TRANSPORTER		2157.226	7942.19	3.682	L17P17F09F1
E1456	1172599	PROTEASOME COMPONENT C5 (MULTICATALYTIC	1354.484	4936.34	3.644	L18P6H10,L35P115A10
E2556			332.316	1204.56	3.625	L22P8G08,L35P96C04
E4344	G763		384.422	1389.72	3.615	J121F03F1
E1440	4512699	(AC006569) putative NADH-ubiquinone oxireductase... +1	1111.552	4015.72	3.613	L20P14F06,L35P115F06
E4384	G776		425.665	1536.04	3.609	J121F05F1
E2531	3461828	(AC004138) unknown protein [Arabidopsis thaliana] +1	314.317	1133.59	3.607	L15P7A12,L35P77G09
E4110	GP-39		88.862	319.55	3.596	O17204,M80927
E3216	453292	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] +3	2410.474	8595.02	3.566	L15P4C04,L35P101D12
E1223			650.996	2311.43	3.551	L18P20F12,L35P113B03
E4192	A.thaliana	transcriptional activator CBF1 mRNA,	186.288	661.31	3.55	O17292,U77378
E718	2499087	UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE	407.89	1446.34	3.546	L18P15F01,L35P87G03
E146	G364		701.002	2473.11	3.528	L17P16D07,L35P81G05
E2325	4585972	(AC005287) Putative ATPase [Arabidopsis thaliana] +1	2996.723	10561.28	3.524	L22P17B04,L35P94B10
E3554	4185509	(AF102821) actin depolymerizing factor 3 [Arabidopsis thaliana] +3	3414.023	12001.92	3.515	L16P5E08,L35P105E05
E2527	464720	40S RIBOSOMAL PROTEIN S28 >gj 409184 (L09755) .	872.25	3063	3.512	L15P6B11,L35P77F11
E646			559.648	1964.75	3.511	L17P41E06,L35P86C09
E4378	G531		770.846	2704.94	3.509	J121D07F1
E2112	G286		507.529	1776.56	3.5	L20P4B03,L35P92F06
E1412			1130.309	3937.24	3.483	L18P7D04,L35P115B02
E3685	121902	HISTONE H1.1 >pir HSMU11 histone H1.1 - Arabidopsis thaliana] +3	1460.96	5088.71	3.483	L17P14A11,L35P107A04
E3734			4091.01	14247.47	3.483	L17P16A04,L35P107C11
E3827	2245110	(Z97343) hypothetical protein [Arabidopsis thaliana] +2	3335.328	11608.54	3.48	L17P1F08,L35P108F07
E1066	1922937	(AC000106) Similar to Glycine SRC2 (gb AB00013... +2	1858.931	6440.95	3.465	L17P3D04,L35P111B01
E2008	4455800	(Z97343) unnamed protein product [Arabidopsis thaliana] +3	3758.657	13010.92	3.462	L20P13E01,L35P91E04
E1414	4263710	(AC006223) (TF not in Tfgene) HOX-like? putative protein	1261.321	4353.59	3.452	L18P7G02,L35P115B04
E3856			887.986	3061.63	3.448	L17P22D03,L35P109C03

E1419	2341034 (AC000104) F19P19.13 [Arabidopsis thaliana]	+1	4039.798	13926.87	3.447	L18P9E05,L35P115C03
E3922	1086263 TMV resistance protein N - tobacco (Nicotiana ...)	+3	581.425	2002.08	3.443	L17P25H03,L35P109F09
E1818	2129733 serine O-acetyltransferase (EC 2.3.1.30) SAT1 ...	+1	3754.306	12918.94	3.441	L24P9D03,L35P119E06
E4922	G313		351.309	1198.38	3.411	J127F12F1
E717	3860163 (AF098962) disease resistance protein RPP1-WsA...+		2390.599	8152.61	3.41	L18P15E01,L35P87G02
E3584	4263698 (AC006223) unknown protein [Arabidopsis thaliana] +2		3183.819	10836.92	3.404	L16P6F09,L35P105H10
E1067	4263712 (AC006223) putative ribosomal protein S12 [Ara... +3]		1747.757	5921.72	3.388	L17P3D05,L35P111B02
E6869			1054.3	3566.42	3.383	J47G05F1
E1820	510730 (L27087) nitrate reductase [Artificial gene] +2	232	1176.499	3970.87	3.375	L28P1D08,L35P119F02
E1559	2244869 (Z97337) hypothetical protein [Arabidopsis thal... +2	35	514.614	1728.79	3.359	L20P2E02,L35P116B11
E4575	G1275		245.182	823.45	3.359	J123F05F1
E3692	4510363 (AC007017) putative DNA-binding protein [Arabi... +3]		1717.776	5752.91	3.349	L17P14G05,L35P107B05
E76	4678328 (AL049658) aldehyde dehydrogenase (NAD+)-like ... +2		2872.597	9619.28	3.349	L16P7G07,L35P80D07
E4364	G43		1187.96	3978	3.349	J121A05F1
E4003	isocitrate dehydrogenase		530.574	1775.13	3.346	L15P4E04F1
E1507	132939 60S RIBOSOMAL PROTEIN L3 >pir JQ0771 ribosoma.		1524.216	5097.01	3.344	L20P1E03,L35P116B01
E3717			2832.274	9469.4	3.343	L17P17F02,L35P107H06
E2251			1323.509	4421.93	3.341	L22P11C08,L35P93F07
E3730			2326.41	7772.23	3.341	L17P15G10,L35P107C07
E1078	231683 CALNEXIN HOMOLOG PRECURSOR >pir JN0597 cal		1459.493	4873.94	3.339	L17P41E07,L35P111D01
E346			878.49	2914.07	3.317	L17P20G03,L35P83A08
E3420	4689436 (AF143096) peptidyl-prolyl cis-trans isomerase... +3	2	1614.557	5355.69	3.317	L15P9E08,L35P103D02
E809	3193289 (AF069298) similar to several small proteins (... +3	13	864.805	2864.04	3.312	L18P27E05,L35P88F05
E4325	G533		1409.002	4662.43	3.309	J121D09F1
E766			697.82	2307.46	3.307	L18P17B01,L35P87G10
E1663	4454019 (AL035396) SRG1-like protein(dioxygenase- ethylene		569.244	1881.89	3.306	L22P1C08,L35P117D07
E3735	3421123 (AF043538) 20S proteasome beta subunit PBG1 [A... +		1704.525	5632.2	3.304	L17P16A07,L35P107C12
E3934	3204125 (AJ006766) putative Pi starvation-induced prot... +3	3	400.358	1318.75	3.294	L17P27G08,L35P109H09
E3296	2781394 (UJ0424) O-methyltransferase 1 [Arabidopsis th... +3]		1474.695	4854.49	3.292	L34P4G06,L35P120D08
E1099	3298540 (AC004681) unknown protein [Arabidopsis thaliana] +1		669.604	2202.89	3.29	L17P6H07,L35P111H04
E2857	4455210 (AL035440) putative aspartate-tRNA ligase [Ara... +3]		813.021	2670.01	3.284	L16P5D02,L35P79G01
E1665	3790587 (AF079182)(Ring finger not in Tfgene) RING-H2 finger		2269.208	7443.96	3.28	L22P1D05,L35P117D09
E670	3548818 (AC005313) unknown protein [Arabidopsis thaliana] +2		1471.898	4827.59	3.28	L17P7B05,L35P86G09
E4057	glutamate--ammonia ligase		741.002	2427.19	3.276	L20P2E04F1
E3388	4490705 (AL035680) ribosomal protein L14-like protein ... +1	1	921.759	3014.99	3.271	L15P7G03,L35P102F09
E3689			2780.863	9067.83	3.261	L17P14E11,L35P107B02
E4921	G512		275.648	897.92	3.257	J127F04F1

E719	3128217 (AC004077) hypothetical protein [Arabidopsis t... +1 74	1158.737	3769.54	3.253	L18P15F04,L35P87G04
E3161	99772 ubiquitin 81-aa extension protein 2 - Arabidop... +1 742	870.311	2826.04	3.247	L15P3H01,L35P101C05
E4444	G371	788.273	2557.23	3.244	J122C09F1
E2090	2827714 (AL021684) receptor protein kinase - like prot... +1 19	3951.993	12816.77	3.243	L20P1D04,L35P92C02
E4635	G209	532.489	1725.01	3.24	J124C05F1
E3772	4415907 (AC006282) 60S ribosomal protein L24 [Arabidop... +1	1596.285	5159.14	3.232	L17P19E08,L35P108D04
E1417	3212854 (AC004005) unknown protein [Arabidopsis thaliana] +1	3668.962	11803.09	3.217	L18P9C10,L35P115C01
E3228	3395756 (U76297) plantacyanin [Arabidopsis thaliana] >... +1 5	1760.945	5648.46	3.208	L15P4F10,L35P101F12
E3722		1305.348	4180.1	3.202	L17P14E03,L35P107A11
E854		1214.734	3888.29	3.201	L18P27G01,L35P88F08
E1289	2281631 (AF003096) AP2 domain containing protein RAP2.... +1	2186.585	6986.49	3.195	L18P29A07,L35P113E09
E3807	1076364 pathogen-inducible protein CXc750 precursor - ... +1 4	5930.997	18923.79	3.191	L17P18G04,L35P108B10
E1463	2062164 (AC001645) jasmonate inducible protein isolog ... +2 3	1772.878	5653.96	3.189	L18P9A09,L35P115B11
E1619	2497953 MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN I	806.495	2565.48	3.181	L22P1B09,L35P117D05
E1155	4531445 (AC006224) unknown protein [Arabidopsis thaliana] +3	636.055	2018.59	3.174	L18P10D05,L35P112F01
E3697	2132017 (Ring finger not in Tfgene)hypothetical protein YOL13	1358.499	4308.42	3.171	L17P15F03,L35P107C04
E2690	3335363 (AC003028) hypothetical protein [Arabidopsis t... +1 4	1173.118	3708.95	3.162	L15P8E09,L35P78B11
E1307	3702317 (AC005397) unknown protein [Arabidopsis thalia... +2	1429.785	4518.98	3.161	L18P30C07,L35P113H09
E2911	2244798 (Z97336) hypothetical protein [Arabidopsis tha... +3 62	1706.837	5389.83	3.158	L16P5H07,L35P79H07
E673	4415940 (AC006418) hypothetical protein [Arabidopsis t... +2 3	1800.535	5683.14	3.156	L17P7B12,L35P86G12
E4908	G207	185.282	583.94	3.152	J127E09F1
E2048		478.257	1505.45	3.148	L20P12H02,L35P91D08
E845		1821.976	5725.94	3.143	L18P26F09,L35P88D11
E4983	G1237	969.652	3046.05	3.141	J128D01F1
E4664	G553	1121.248	3516.02	3.136	J124F11F1
E2742		349.022	1092.1	3.129	L23P3C12,L35P97C03
E3131		1719.006	5375.91	3.127	L34P2B07,L35P99F11
E2864		1254.037	3903.64	3.113	L16P5F09,L35P79H02
E2548	4753652 (AL049751) short-chain alcohol dehydrogenase l... +3	2816.724	8750.07	3.106	L22P8D01,L35P96B02
E2907		2297.25	7128.69	3.103	L16P5E10,L35P79G09
E3227	4581173 (AC006220) putative glycine-rich protein [Arab... +2 63	623.302	1929.42	3.095	L15P4F06,L35P101F11
E1603		917.657	2828.78	3.083	L22P12D07,L35P117B01
E529	3548818 (AC005313) unknown protein [Arabidopsis thaliana] +2	1611.586	4954.47	3.074	L17P39E08,L35P85G06
E1847	G899	1718.845	5280.74	3.072	L24P1C01,L35P119B11
E1532		490.786	1506.01	3.069	L21P1A09,L35P116F02
E3527	2244904 (Z97339) similar to hypothetical protein C02F5... +1 3	1675.775	5139.19	3.067	L16P1G10,L35P104D11
E4758	G899	415.821	1274.46	3.065	J125C08F1

E3857	3776578 (AC005388) ESTs gb F13915 and gb F13916 come f...	302.534	926.45	3.062	L17P22D08,L35P109C04
E748	2245108 (Z97343) EREBP-4 homolog [Arabidopsis thaliana] +3	416.392	1274.27	3.06	L18P10D06,L35P87D10
E4039	HIGH AFFINITY AMMONIUM TRANSPORTER	1794.692	5491.37	3.06	L17P17F09F1
E1840	1171991 PHENYLALANINE AMMONIA-LYASE 1 >pir S52990 p	1084.554	3315.95	3.057	L23P8E04,L35P119A10
E2126	G348	3171.053	9680.43	3.053	L20P17D07,L35P92A08
E3468	G654	1263.584	3849.59	3.047	L15P9G04,L35P103D08
E3467	2570507 (AF022736) ribosomal protein [Oryza sativa] +2 43	2305.627	7007.73	3.039	L15P9G03,L35P103D07
E2100	4371290 (AC006260) unknown protein [Arabidopsis thaliana] +3	3297.989	10018.34	3.038	L20P2A12,L35P92D06
E3176	4115925 (AF118222) contains similarity to RNA recognit... +3 4	3331.189	10105.85	3.034	L15P4D11,L35P101F02
E1458	1708924 MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME)	3169.81	9614.02	3.033	L18P7C03,L35P115A12
E1421	2253010 (Y14199) MAP3K delta-1 protein kinase [Arabido... +2	909.925	2759.05	3.032	L18P9G03,L35P115C05
E4067	Actin2	1700.001	5152.09	3.031	L33P3E02F1
E1425	1657621 (U72505) G6p [Arabidopsis thaliana] >gj 306871... +3	1699.504	5147.83	3.029	L20P11E05,L35P115D03
E3724	1709446 PYRUVATE DEHYDROGENASE E1 COMPONENT, A	2022.099	6118.54	3.026	L17P15B11,L35P107B07
E568		236.12	714.07	3.024	L17P39B01,L35P85F09
E535	2244816 (Z97336) hypothetical protein [Arabidopsis tha... +2 33	2402.209	7259.04	3.022	L17P3C04,L35P85H06
E3886	2642215 (AF030386) NOI protein [Arabidopsis thaliana] +1 2	1053.877	3184.1	3.021	L17P27C06,L35P109H03
E3416		2568.982	7746.71	3.015	L15P9B06,L35P103C04
E2420		1395.69	4204.52	3.013	L22P3A12,L35P95D12
E4340	G1045	202.41	607.62	3.002	J121F01F1
E3406	400515 NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT	1498.349	4496.92	3.001	L15P8F02,L35P103A06
E3285	3805847 (AL031986) putative protein [Arabidopsis thali... +1 24	882.927	2649.39	3.001	L34P1D11,L35P120B09
E953	3250675 (AL024486) putative protein [Arabidopsis thali... +3 17	2101.751	6298.87	2.997	L18P33B03,L35P89F11
E5664		1128.929	3383.02	2.997	J27D01F1
E3188	99697 glutamate--ammonia ligase (EC 6.3.1.2), cyto... +2 3	4552.125	13639	2.996	L15P4H11,L35P101H02
E2110	2781362 (AC003113) F24O1.18 [Arabidopsis thaliana] +2 5	1437.193	4299.38	2.992	L20P2H05,L35P92F04
E3178	3811007 (AB019327) NADP specific isocitrate dehydrogen... +2	4356.614	12977.44	2.979	L15P4E04,L35P101F04
E3443	2529229 (AB007907) 6-phosphogluconate dehydrogenase [G... +	2031.72	6044.5	2.975	L16P11B01,L35P103H01
E536	465820 HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHRC	2104.883	6257.66	2.973	L17P30F01,L35P85A07
E4353	G941	1220.253	3626.06	2.972	J121G11F1
E3828		3540.908	10517.83	2.97	L17P1F11,L35P108F08
E4011	gst6	453.832	1348.04	2.97	L15P9B01F1
E1480	137465 VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE	598.703	1771.63	2.959	L20P14C03,L35P115E10
E1490		1304.652	3854.67	2.955	L20P16E04,L35P115G08
E1577	1755178 (U75200) germin-like protein [Arabidopsis thal... +3 43	1932.056	5706.99	2.954	L20P9C08,L35P116E11
E3448	1755156 (U75189) germin-like protein [Arabidopsis thal... +1 36	3780.894	11130.29	2.944	L16P11D06,L35P103H06
E3858	G398	624.147	1837.36	2.944	L17P22E01,L35P109C05

E2854			946.209	2783.86	2.942	L16P5B09,L35P79F04
E2916			983.61	2888.54	2.937	L16P6A09,L35P79H12
E1423	1944132 (AB002560) CUC2 [Arabidopsis thaliana]	+3 49	1162.279	3407.1	2.931	L20P11C07,L35P115D01
E3838	3860261 (AC005824) putative acidic ribosomal protein [...]	+1 34	5806.561	16985.7	2.925	L17P20H07,L35P108H07
E4638	G233		173.361	505.46	2.916	J124C10F1
E3481	1710530 60S RIBOSOMAL PROTEIN L27A >pir S71256 riboso.		3085.137	8992.64	2.915	L16P10F06,L35P103F09
E4007	CYSTEINE PROTEINASE 2 PRECURSOR		712.487	2074.54	2.912	L15P6D02F1
E2487	3915085 TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAM		982.144	2856.35	2.908	L15P7C08,L35P77H01
E3702	3297815 (AL031032) putative protein [Arabidopsis thali...	+1 21	1310.992	3804.44	2.902	L17P16C03,L35P107D04
E1482			511.084	1482.83	2.901	L20P14D05,L35P115E12
E3549	2160158 (AC000132) Similar to elongation factor 1-gamm...	+3	4501.635	13005.37	2.889	L16P5A10,L35P105C02
E598	4678953 (AL049711) hypothetical protein fragment [Arab...	+1 1	680.915	1965.11	2.886	L17P41B02,L35P86C03
E4053	endochitinase		479.972	1382.99	2.881	L18P8B07F1
E3137	3915824 [Segment 2 of 2] 60S RIBOSOMAL PROTEIN L5		3074.236	8841.26	2.876	L34P2G04,L35P99G11
E3575	2052379 (U66343) calreticulin [Arabidopsis thaliana]	+3 126	2664.258	7654.61	2.873	L16P5G06,L35P105F09
E1193	1169383 DNAJ PROTEIN HOMOLOG ATJ >gil 535588 (L36113)		989.204	2839.67	2.871	L18P10A08,L35P112E09
E4524	G1093		641.649	1840.94	2.869	J123E09F1
E1218	4559385 (AC006526) putative cyclic nucleotide-regulate...	+1 6	1994.48	5716.23	2.866	L18P1B12,L35P113A04
E2791	461729 10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN G		1168.569	3342.22	2.86	L23P5H05,L35P97C10
E1825	872030 (X88774) aspartic protease [Brassica oleracea]	+2 1	1995.636	5700.46	2.856	L28P2C03,L35P119G01
E1473	4204263 (AC005223) 40409 [Arabidopsis thaliana]	+3 36	749.293	2139.94	2.856	L20P12D03,L35P115D09
E612			623.439	1778.85	2.853	L17P5C10,L35P86E05
E2800			497.709	1414.07	2.841	L23P9G02,L35P97E08
E4549	G1390		159.539	453.02	2.84	J123H02F1
E2790	1362162 beta-glucosidase BGQ60 precursor - barley >gil... +2		2489.43	7066.2	2.838	L23P5H03,L35P97C09
E3540	399013 ADP.ATP CARRIER PROTEIN 1 PRECURSOR (ADP/A		3505.42	9943.93	2.837	L16P2E10,L35P104H11
E1616	4510370 (AC007017) unknown protein [Arabidopsis thaliana]	+1	1090.807	3090.69	2.833	L22P19C07,L35P117D02
E702			1175.38	3321.19	2.826	L18P10B06,L35P87D05
E1827	3510254 (AC005310) putative zinc transporter [Arabidop...	+3 3	816.439	2306.84	2.825	L28P2D03,L35P119G03
E1957			1226.194	3462.2	2.824	L18P5F10,L35P90E07
E1595	2506276 RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUB		1384.018	3895.05	2.814	L22P10D03,L35P116H11
E3531	3168840 (U88711) copper homeostasis factor [Arabidopsi...	+1	2531.493	7123.13	2.814	L16P2B04,L35P104F07
E2607			893.754	2514.19	2.813	L22P9E04,L35P96D08
E4391	G1039		431.035	1210.14	2.808	J121H05F1
E1437			898.738	2522.5	2.807	L20P14D08,L35P115F03
E4563			255.486	716.56	2.805	J123C05F1
E1448			1005.686	2816.55	2.801	L20P17A06,L35P115H02

E1527	3128183 (AC004521) unknown protein [Arabidopsis thaliana] +2	907.775	2538.13	2.796	L20P7D01,L35P116E03
E3936		839.721	2338.04	2.784	L17P27G11,L35P109H11
E6736	3851530 (AF065435) nodulin [Glycine max] +2 408 ;	664.122	1847.63	2.782	J46B06F1
E4844	G1006	1305.547	3628.05	2.779	J126E09F1
E747		2233.173	6203.53	2.778	L18P10C02,L35P87D09
E3546	4314378 (AC006232) putative lipase [Arabidopsis thaliana] +1 ;	1867.57	5176.78	2.772	L16P2H03,L35P105B05
E3490	2146733 GAST1 protein homolog (GA reg gene)(clone GASA1)	1360.823	3767.92	2.769	L16P10H12,L35P103G12
E3726	3249099 (AC003114) EST gb T21244 comes from this gene... +	891.231	2466.9	2.768	L17P15D01,L35P107B09
E1230	2058282 (X97377) atranbp1a(bind GTPbinding proteins - cell	1078.886	2983.74	2.766	L18P25D09,L35P113C04
E2887	2914704 (AC003974) unknown protein [Arabidopsis thaliana] +1	1510.841	4170.37	2.76	L16P2E05,L35P79D07
E1348	3021270 (AL022347) serine/threonine kinase -like prote... +3 6	1454.956	4008.92	2.755	L18P4H10,L35P114G03
E4699	G735	178.122	489.19	2.746	J125C01F1
E1264	2347098 (U76845) ubiquitin-specific protease [Arabidop... +2 6	681.039	1864.41	2.738	L18P1G02,L35P113A08
E673	4415940 (AC006418) hypothetical protein [Arabidopsis t... +2 3	3398.112	9291.32	2.734	L17P7B12,L35P86G12
E4003	isocitrate dehydrogenase	493.061	1347.51	2.733	L15P4E04F1
E1410	3426062 (AJ007587) monooxygenase [Arabidopsis thaliana] +2	1716.085	4685.91	2.731	L18P6E11,L35P115A06
E1444	3451072 (AL031326) putative protein [Arabidopsis thali... +3 46	1672.133	4559.79	2.727	L20P15G08,L35P115G04
E1081	2970654 (AF052058) ferritin subunit cowpea2 precursor ... +3 4	420.556	1146.25	2.726	L17P41G03,L35P111D06
E3424	730456 40S RIBOSOMAL PROTEIN S19 +3 42	2352.986	6409.27	2.724	L15P9F09,L35P103D06
E3488	4567232 (AC007119) putative 40S ribosomal protein S25 ... +2	3590.379	9772.63	2.722	L16P10H07,L35P103G10
E5133	G322	577.411	1569.34	2.718	J129B05F1
E4407	G353	866.458	2354.51	2.717	J122D01F1
E2378		2543.14	6904.62	2.715	L22P3E03,L35P95E01
E5338		320.333	869.49	2.714	J56G06F1
E3564	1706958 (U58284) cellulose synthase [Gossypium hirsutum] +1	518.144	1406.26	2.714	L16P6E06,L35P105H05
E6574		1074.685	2911.7	2.709	J44F02F1
E4305	G277	1017.196	2754.86	2.708	J121A11F1
E2132		2149.457	5819.23	2.707	L20P1B11,L35P92B08
E3428	3164140 (D78605) cytochrome P450 monooxygenase [Arabid...	1290.333	3489.23	2.704	L16P10A04,L35P103E04
E3723	3135264 (AC003058) unknown protein [Arabidopsis thaliana] +3	835.184	2257.03	2.702	L17P14E05,L35P107A12
E1821		1017.395	2740.28	2.693	L28P1D11,L35P119F03
E2765	4467147 (AL035540) putative protein [Arabidopsis thali... +1 24	2205.206	5936.13	2.692	L24P1C02,L35P97G02
E832	1717952 UBIQUINOL-CYTOCHROME C REDUCTASE IRON-S	2177.598	5858.84	2.691	L18P23C05,L35P88B10
E2023	4371290 (AC006260) unknown protein [Arabidopsis thaliana] +2	2266.386	6092.06	2.688	L20P15H06,L35P91H01
E2308		1950.366	5238.59	2.686	L22P21D05,L35P94G04
E2266		2112.627	5664.69	2.681	L22P13G01,L35P93H10
E3712	1350956 40S RIBOSOMAL PROTEIN S20 (S22) +2	2071.695	5552.77	2.68	L17P17B07,L35P107G06

E2904	3096947 (Y16327) putative cyclic nucleotide-regulated ... +3	2032.429	5445.27	2.679	L16P5D01,L35P79F12
E3879	3122673 60S RIBOSOMAL PROTEIN L15 >emb CAB10447 (ZS	1519.455	4064.16	2.675	L17P26D06,L35P109G02
E3751		2627.801	7024.33	2.673	L17P17G08,L35P107H12
E2753		1120.875	2995.42	2.672	L23P9B02,L35P97E02
E6564	464621 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >pir S28..	686.857	1833.65	2.67	J44D08F1
E256	1903360 (AC000104) Similar to Arabidopsis 2A6 (gb X830... +1	2086.524	5568.25	2.669	L17P17G01,L35P82B07
E2423		2174.23	5802.16	2.669	L22P4B05,L35P95E09
E3412		751.232	2001.82	2.665	L15P8H02,L35P103B06
E4707	G911	193.038	513.68	2.661	J125D01F1
E4470	G1351	829.267	2205.63	2.66	J122F10F1
E3861		511.979	1359.81	2.656	L17P23D01,L35P109D02
E3287		1726.464	4578.97	2.652	L34P1E05,L35P120B11
E3854	480450 ketol-acid reductoisomerase (EC 1.1.1.86) - Ar... +3	1481.27	3912.48	2.641	L17P22B12,L35P109C01
E2099		1188.879	3138.16	2.64	L20P2A10,L35P92D05
E3719		1920.981	5051.66	2.63	L17P14D04,L35P107A08
E3418		1972.392	5184.41	2.628	L15P9B10,L35P103C06
E3426	2864622 (AL021811) putative protein [Arabidopsis thali... +1	4130.401	10856.46	2.628	L15P9H12,L35P103E02
E2380	4539459 (AL049500) putative protein [Arabidopsis thali... +1	1693.624	4449.13	2.627	L22P3F08,L35P95E03
E1295	452470 (U05218) ATP sulfurylase [Arabidopsis thaliana] +2	4274.477	11223.26	2.626	L18P29H08,L35P113F09
E3862		1473.501	3864.24	2.622	L17P23D11,L35P109D03
E3880	3702327 (AC005397) unknown protein [Arabidopsis thaliana] +2	2417.112	6336.64	2.622	L17P26E12,L35P109G03
E711		646.472	1693.56	2.62	L18P11D02,L35P87F02
E3598	4678921 (AL049711) putative calmodulin [Arabidopsis th... +1	3605.817	9443.29	2.619	L16P7D12,L35P106B06
E4633	G508	1738.583	4544.03	2.614	J124B08F1
E716	3309082 (AF076251) calcineurin B-like protein 1 [Arabi... +3	473.819	1238.14	2.613	L18P15D12,L35P87G01
E2892		4196.404	10964.88	2.613	L16P2F08,L35P79D12
E2203	G483	578.79	1511.63	2.612	L22P10H06,L35P93F01
E1854		1637.478	4268.05	2.606	L24P5E01,L35P119C12
E2856		1777.328	4632.29	2.606	L16P5B12,L35P79F06
E715	G1334	515.459	1343.15	2.606	L18P12A12,L35P87F06
E3263	1806140 (X97314) cdc2MsC [Medicago sativa]	1475.378	3844.44	2.606	L34P3H08,L35P120D05
E4471	G284	975.867	2542.47	2.605	J122F07F1
E3116	1532169 (U63815) similar to a E. coli hypothetical pro... +1	924.667	2408.79	2.605	L33P8F02,L35P99D08
E5140	G411	2882.292	7494.38	2.6	J129C08F1
E5312		343.627	892.57	2.597	J56D05F1
E5465	4587529 (AC007060) Strong similarity to F19I3.2 gi 303... +1	329.656	856.15	2.597	J19C09F1
E2754	2980766 (AL022198) putative calmodulin-binding protein... +2	1149.054	2984.06	2.597	L23P9D03,L35P97E03

E4053	endochitinase	402.21	1042.29	2.591	L18P8B07F1
E2018		1471.6	3813.27	2.591	L20P14G07,L35P91G02
E3737	3687235 (AC005169) putative copia-like transposable el...	2404.197	6226.42	2.59	L17P16F06,L35P107E08
E784	3420008 (AF000307) steroid sulfotransferase 3 [Brassic...	2963.075	7671.23	2.589	L18P20G12,L35P88B04
E2257		1202.714	3112.11	2.588	L22P12E07,L35P93G07
E4416	G776	474.987	1228.24	2.586	J122F02F1
E528	3329368 (AF031244) nodulin-like protein [Arabidopsis t...	1069.626	2765.63	2.586	L17P39E05,L35P85G05
E1134	445612 ribosomal protein S19 [Solanum tuberosum]	1495.627	3848.45	2.573	L17P7C04,L35P112A05
E1874		876.538	2255.41	2.573	L28P3A08,L35P119G08
E4739	G1029	530.102	1358.63	2.563	J125H01F1
E4069	caffeic o-methyltransferase	561.6	1438.48	2.561	L34P4G06F1
E754		616.49	1577.41	2.559	L18P11A03,L35P87E10
E1597	419757 ketol-acid reductoisomerase (EC 1.1.1.86) prec...	2092.316	5350.57	2.557	L22P10H08,L35P117A01
E2238		3299.219	8418.19	2.552	L21P5F05,L35P93C12
E3714	484656 monodehydroascorbate reductase (NADH) (EC 1.6....	4129.406	10536.21	2.552	L17P17E01,L35P107H03
E3191	3023858 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA S	1779.578	4538.78	2.55	L15P5A02,L35P101H05
E5157		268.749	685.31	2.55	J129H05F1
E1811		1415.702	3606.26	2.547	L24P5H10,L35P119D05
E3343	4753651 (AL049751) ribosomal protein L13a like protein...	3606.265	9185.06	2.547	L15P7E08,L35P102F06
E1459	2281112 (AC002333) endochitinase isolog [Arabidopsis t...	678.106	1725.3	2.544	L18P8B07,L35P115B07
E1610	3786008 (AC005499) unknown protein [Arabidopsis thaliana]	953.294	2420.03	2.539	L22P14H01,L35P117C02
E6399	2633544 (Z99110) yjgL [Bacillus subtilis]	634.017	1607.69	2.536	J42H06F1
E3189	2129570 DAD-1 homolog - Arabidopsis thaliana >emb CAA6...	2181.924	5526.96	2.533	L15P4H12,L35P101H03
E4518	G1050	463.428	1173.38	2.532	J123D10F1
E3181	3395427 (AC004683) unknown protein [Arabidopsis thaliana]	1499.406	3793.28	2.53	L15P4F11,L35P101G01
E2426	3023522 COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN	1005.363	2541.11	2.528	L22P5E06,L35P95E12
E2209		1431.438	3613.57	2.524	L22P11G02,L35P93G01
E4314	G321	1096.835	2766.48	2.522	J121B04F1
E2629		2178.208	5492.76	2.522	L23P1G12,L35P96H10
E1442	4678328 (AL049658) aldehyde dehydrogenase (NAD+)-like ...	3511.188	8846.47	2.52	L20P15F07,L35P115G02
E2010	3157937 (AC002131) identical to aspartic proteinase cD...	5679.911	14308.81	2.519	L20P14A03,L35P91E06
E1015	2493052 ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL	2206.113	5557.42	2.519	L17P28F10,L35P110A09
E2058		402.719	1014.18	2.518	L20P14C02,L35P91E12
E0	NUL	623.812	1570.11	2.517	NUL
E744	3915710 G-BOX BINDING FACTOR 1 >emb CAA68197 (X9994	272.341	685.09	2.516	L18P10B11,L35P87C11
E761	3395441 (AC004683) unknown protein [Arabidopsis thaliana]	1720.05	4321.36	2.512	L18P15C10,L35P87F11
E200	1402900 (X98322) peroxidase [Arabidopsis thaliana] >em...	562.321	1412.4	2.512	L17P17B05,L35P81H11

E5503	2708749 (AC003952) putative senescence-assoc. rhodanes...	+2	216	989.448	333.29	2.969	1	4	3
E6511	3033375 (AC004238) putative berberine bridge enzyme [A...	+3	285	1592.617	536.91	2.966	1	1	5
E2531	3461828 (AC004138) unknown protein [Arabidopsis thaliana]	+1	158	1901.73	641.75	2.963	1	1	8
E1112	2245066 (Z97342) Beta-Amylase [Arabidopsis thaliana]	+2	360	9207.632	3110.64	2.96	2	3	16
E2266	G713			1933.051	653.46	2.958	3	3	12
E4693				1065.144	361.56	2.946	3	3	20
E5554				1371.105	465.6	2.945	2	1	2
E1458	1708924 MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NAC			4696.698	1599.93	2.936	2	3	17
E1308	499301 (X77116) ABI1 [Arabidopsis thaliana] >gi54998...	+1	351	11733.7	3996.48	2.936	3	3	18
E5632	1170034 GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-			13616.3	4638.57	2.935	4	1	3
E1220	2894563 (AL021890) putative protein [Arabidopsis thali...	+1	293	3204.744	1100.29	2.913	1	3	17
E5509	3549656 (AL031394) putative protein [Arabidopsis thali...	+2	636	1931.032	664.54	2.906	3	2	3
E5373	1169544 ERD1 PROTEIN PRECURSOR >pir JN0901 ERD1 prote...	+		9629.566	3335.98	2.887	3	3	2
E1027				1028.897	356.99	2.882	1	2	16
E1868	4678332 (AL049658) putative peptide transporter [Arabi...	+3	311	3.2	2644.26	2.873	4	3	19
E5386	99698 glutamate--ammonia ligase (EC 6.3.1.2), cyto...	+2	966	1.5	306.08	2.868	1	1	2
E5448	4105633 (AF048982) putative ethylene receptor [Arabi...	+3	902	1.	312.97	2.866	1	1	2
E5802	2642446 (AC002391) similar to auxin-responsive GH3 pro...	+1	225	2372.087	830.55	2.856	1	1	3
E5608	4581500 (AL034352) putative oxalyl-CoA decarboxylase [...]	+1	93	7.	600.81	2.853	2	1	2
E3696	629602 probable imbibition protein - wild cabbage >em...	+3	514	3.8	935.77	2.852	2	1	15
E5095	G515			1336.354	469.56	2.846	3	1	22
E5960	2924517 (AL022023) putative protein [Arabidopsis thali...	+3	379	1.8	780.94	2.845	2	3	3
E4050	pathogen-inducible protein CXc750			2500.776	879.76	2.843	1	2	1
E1477	1170034 GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-			4767.409	1680.95	2.836	2	1	18
E2706				16428.07	5792.45	2.836	1	2	8
E6038	G350			2627.057	927.84	2.831	2	2	3
E3325				2655.379	940.4	2.824	1	4	14
E5067				790.707	281.19	2.812	1	1	21
E2396	1076261 beta-fructofuranosidase (EC 3.2.1.26) - red go...	+2	231	5.2	1721.56	2.811	4	1	12
E3686	4469007 (AL035602) UDP rhamnose-anthocyanidin-3-glucos...	+2	67		1547.9	2.81	2	1	15
E2343	541849 anthranilate synthase (EC 4.1.3.27) beta chain...	+3	367	1.9	2019.47	2.799	1	2	12
E6633	3341680 (AC003672) unknown protein [Arabidopsis thaliana]	+3	293		415.93	2.798	1	2	5
E4006	VACUOLAR ATP SYNTHASE			704.238	252.33	2.791	1	1	1
E3313	464367 POLYGALACTURONASE INHIBITOR PRECURSOR (POLYC			1651.398	592.34	2.788	1	4	14
E4731	G860			608.948	218.8	2.783	1	1	21
E605	4689366 (AF134155) RING finger protein [Arabidopsis th...	+3	294	3.	2835.92	2.783	4	1	16
E2355	2894607 (AL021889) NAM (no apical meristem) - like pro...	+1	186	3	1414.77	2.782	1	2	12

E6058	2959736 (Y13651) homologous to GATA-binding transcript... +3	148	651.211	234.43	2.778	2	2	3
E5378	2500981 GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIC		1263.362	455.1	2.776	1	1	2
E4218			2364.246	852	2.775	3	2	22
E6104	4417286 (AC007019) putative shikimate kinase [Arabidop... +3	345	1	781.675	2.767	2	2	3
E648	1946361 (U93215) C3HC4 zinc finger protein isolog [Ara... +1	973	3	328.689	2.765	1	2	10
E6933	3522935 (AC004411) putative alcohol dehydrogenase [Ara... +1	589		350.024	2.765	1	1	7
E5280	4337198 (AC006403) putative auxin-induced protein [Ara... +1	905	5	584.691	2.765	2	1	7
E3204	3763924 (AC004450) putative extensin [Arabidopsis thal... +3	270	1	1575.803	2.764	3	3	14
E5465	4587529 (AC007060) Strong similarity to F1913.2 gl[303... +1	338	6	1459.146	2.759	1	2	2
E2478	4432856 (AC006300) putative 2A6 protein [Arabidopsis t... +1	125	3	5219.338	2.753	3	3	8
E4569	G1308		713.836	259.89	2.747	4	1	19
E106	4504085 glycerol-3-phosphate dehydrogenase 2 (mitochon... +2	152		999.13	2.747	1	1	8
E2178			632.505	230.3	2.746	1	3	12
E1078	231683 CALNEXIN HOMOLOG PRECURSOR >pir JN0597 calnex...		12668.82	4629.05	2.737	4	1	16
E6813	4587607 (AC006951) putative antisense basic fibroblast... +1	524	9	639.23	2.729	2	2	6
E5134	2117612 catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana	+3	840	2.8	2.728	3	3	21
E5692	3941524 (AF062916) putative transcription factor [Arab... +3	376	3	996.258	2.724	2	2	2
E4005	3' flavonoid O-methyltransferase		3136.753	1152.17	2.722	1	3	1
E6744			1752.881	645.43	2.716	2	3	5
E3266	1684851 (U77935) DnaJ-like protein [Phaseolus vulgaris] +2	188	5	1815.439	2.711	2	4	19
E6736	3851530 (AF065435) nodulin [Glycine max] +2	408	2.6e-3	3454.805	2.711	4	3	5
E4077	6-Human metallothionein-II gene		1718.611	636.62	2.7	2	3	1
E4662	G545		1377.299	510.58	2.698	4	4	20
E1347	2262098 (AC002343) HSP90 isolog [Arabidopsis thaliana] +3	632	2	2096.872	2.695	1	4	18
E2979	2191147 (AF007269) A_IG002N01.26 gene product [Arabido... +1	201		3755.182	2.691	1	2	13
E1229			425.247	158.13	2.689	1	1	17
E7045	2341040 (AC000104) EST gb H76414 comes from this gene.... +2	44		763.188	2.686	1	2	6
E3518	3668173 (AB006777) vegetative storage protein [Arabido... +1	682	1	1696.018	2.681	2	4	14
E5814	2342686 (AC000106) Similar to Saccharomyces hypothetic... +3	798		1232.269	2.68	3	3	3
E2212			626.345	233.89	2.678	1	3	12
E3248	3660471 (AJ001809) succinate dehydrogenase flavoprotei... +3	424	1	5307.817	2.677	4	4	18
E3530	3695019 (AF055848) subtilisin-like protease [Arabidops... +1	349	6.3	7629.209	2.675	2	4	14
E5644	4185144 (AC005724) unknown protein [Arabidopsis thaliana] +2	484		1163.467	2.674	2	2	2
E6199			756.26	282.95	2.673	1	1	4
E5376	2213583 (AC000348) T7N9.3 [Arabidopsis thaliana] +2	138	4.3	3480.508	2.671	1	1	2
E2154	3913518 3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5'-... +3	31		1365.225	2.67	2	4	11
E5132	G179		1290.881	483.58	2.669	1	3	21

E3005	3548819 (AC005313) putative heterogeneous nuclear ribo...	+1	187	1790.125	671.77	2.665	1	2	14
E2309				2922.322	1096.51	2.665	1	2	12
E2354				2233.309	838.32	2.664	1	4	12
E4471	G284			514.03	193.11	2.662	3	2	20
E5312				4525.61	1701.27	2.66	4	1	6
E2042				3984.272	1499.11	2.658	2	3	11
E2444	2578440 (X67425) pectinesterase [Pisum sativum]	+1	147	6018.451	2264.08	2.658	4	3	12
E3463	3123188 CATALASE 3 >gj 2347178 (U43147) catalase 3 [Ar...	+2	45	9507.56	3580.43	2.655	2	1	14
E4006	VACUOLAR ATP SYNTHASE			6967.048	2634.39	2.645	1	2	1
E1003	2262105 (AC002343) unknown protein [Arabidopsis thaliana]	+3	682	460.868	174.3	2.644	1	4	17
E4573	G1080			448.034	169.55	2.642	2	1	20
E4547				506.333	191.66	2.642	4	1	20
E5845	1709798 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG	>		1828.011	692.12	2.641	1	2	3
E2410				1421.691	539.64	2.635	2	3	12
E6137				997.137	378.84	2.632	1	1	4
E7022				1602.038	609.82	2.627	3	2	7
E302	2529229 (AB007907) 6-phosphogluconate dehydrogenase [G...	+1	55	15221.34	5793.24	2.627	2	3	8
E2308				838.031	319.37	2.624	1	4	12
E6269	2118045 beta-fructofuranosidase (EC 3.2.1.26) - Arabid...	+2	929	1913.601	729.23	2.624	3	2	4
E5368	4704730 (AF121355) peroxiredoxin TPx1 [Arabidopsis tha...	+2	655	2157.993	822.48	2.624	1	1	2
E6973				466.259	177.9	2.621	1	1	7
E3624	3859606 (AF104919) contains similarity to cysteine pro...	+1	214	12746.54	4863.44	2.621	1	2	16
E5362	2832677 (AL021712) hypothetical protein [Arabidopsis t...	+2	203	729.29	278.34	2.62	1	1	2
E4005	3' flavonoid O-methyltransferase			1312.004	501.03	2.619	1	4	1
E5858				1368.123	522.95	2.616	3	2	3
E3085				4158.376	1590.74	2.614	2	1	13
E3585	2129769 xyloglucan endo-transglycosylase precursor - A...	+1	756	23791.86	9108.56	2.612	3	1	16
E6373	2511546 (AF022658) putative c2h2 zinc finger transcrip...	+1	351	1177.256	451.09	2.61	2	1	4
E4005	3' flavonoid O-methyltransferase			1768.03	677.96	2.608	2	3	1
E5935				1227.655	471.49	2.604	2	1	3
E2627				3054.771	1174.6	2.601	4	4	12
E5788	2642153 (AC003000) unknown protein [Arabidopsis thalia...	+3	494	520.807	200.31	2.6	1	1	4
E2916				8251.989	3174.27	2.6	3	1	16
E6889	4538929 (AL049483) putative nucleic acid binding prote...	+1	132	1312.916	505.11	2.599	1	1	6
E1714				3910.832	1505.51	2.598	3	4	18
E4026	thionin			1040.371	400.61	2.597	2	1	1
E6525	3128184 (AC004521) unknown protein [Arabidopsis thaliana]	+1	405	608.636	234.58	2.595	1	1	6

E580	541848	amino acid transport protein I - Arabidopsis t...	+3	580	1.6e-1	13797.22	5335.56	2.586	3	1	10
E2503	510876	(X80051) NADP dependent malic enzyme [Phaseolu...	+1	16	5926.541	2292.92	2.585	2.585	3	1	7
E6942	2078350	(U95923) transaldolase [Solanum tuberosum]	+1	330	4	2482.999	961.08	2.584	3	1	7
E2491					4316.73	1671.89	2.582	2.582	3	1	8
E5464	1699053	(U78868) putative aspartate-arginine-rich mRNA...	+2	174	1	1825.392	707.88	2.579	1	2	2
E4279					354.645	137.63	2.577	2.577	3	4	22
E5354	3935145	(AC005106) T25N20.9 [Arabidopsis thaliana]	+1	277	2.	573.369	222.48	2.577	1	1	2
E4179	Cre				2107.205	819.65	2.571	2.571	4	3	22
E6976	2317729	(AF013627) reversibly glycosylated polypeptide...	+2	610	1.	2789.129	1085.83	2.569	1	3	7
E2533					2835.498	1104.34	2.568	2.568	1	1	8
E4565	G926				403.253	157.13	2.566	2.566	2	1	19
E4246	3123712	(D89051) ERD6 protein [Arabidopsis thaliana]	+2	417	2.	3548.067	1384.75	2.562	3	2	21
E96					4805.683	1877	2.56	2.56	2	2	8
E2297	1778095	(U64903) putative sugar transporter; member of...	+3	325	1	5458.931	2135.11	2.557	1	2	12
E4026	thionin				1501.763	587.6	2.556	2.556	1	2	1
E0	NUL				595.142	233.17	2.552	2.552	3	1	22
E4076	5-Human cathepsin O or X mRNA				1714.057	672.03	2.551	2.551	2	1	1
E875	4262242	(AC006200) NADC homolog [Arabidopsis thaliana]	+2	525		3690.816	1448.71	2.548	1	1	10
E1607	2660677	(AC002342) unknown protein [Arabidopsis thaliana]	+2	663		3273.503	1285.46	2.547	3	1	18
E1562	3164138	(D78604) cytochrome p450 monooxygenase [Arabid...	+3	38		1206.6	473.87	2.546	2	4	17
E4077	6-Human metallothionein-II gene				2247.977	882.99	2.546	2.546	1	4	1
E6153	3892722	(AL033545) putative protein [Arabidopsis thali...	+1	262	7.3e	572.516	225.2	2.542	1	1	4
E6247					934.655	367.76	2.541	2.541	1	4	4
E6026					1503.546	591.66	2.541	2.541	2	2	3
E1265	1703220	AIG2 PROTEIN >gij1127806 (U40857) AIG2 [Arabid...	+2	58		1806.111	711.42	2.539	1	1	17
E6503	2894571	(AL021890) putative protein [Arabidopsis thali...	-2	170	7.0e	869.63	343.76	2.53	1	1	5
E0	NUL				593.799	235.64	2.52	2.52	4	1	22
E5968	285286	flavonol 4'-sulfotransferase - Flaveria chlora...	+2	218	3.4e-1	1865.821	740.46	2.52	2	3	3
E6792	629602	probable imbibition protein - wild cabbage >em...	+3	202	2.6	3189.442	1270.93	2.51	2	4	5
E2290					7639.846	3044.15	2.51	2.51	3	4	12
E1739	1817544	(D83025) proline oxidase precursor [Arabidopsi...	+3	493	2.	955.491	381.65	2.504	3	2	19
E2329					2720.775	1087.98	2.501	2.501	1	2	12
E3851	3894183	(AC005662) calmodulin-like protein [Arabidopsi...	+3	462	3.	6627.67	2649.59	2.501	3	3	16
E4358	G1007				555.161	222.04	2.5	2.5	3	3	20
E6145	4038034	(AC005936) unknown protein [Arabidopsis thaliana]	+1	328		5712.592	2286.45	2.498	3	1	4
E4084	14-Human IgSF full-length EST				4422.226	1771.58	2.496	2.496	4	1	1
E5704					7218.334	2891.39	2.496	2.496	2	2	2

E3873	3402700 (AC004261) unknown protein [Arabidopsis thaliana] +1 623	3527.764	1514.31	2.33	3	3	16
E501	4115383 (AC005967) receptor-like protein kinase [Arabi... +1 180 6.4	5532.785	2377.49	2.327	1	1	10
E1015	2493052 ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL >dbj.	2710.298	1165.2	2.326	1	2	16
E6319	1708971 (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR (1208.096	519.57	2.325	2	1	4
E1179	1709794 26S PROTEASOME REGULATORY SUBUNIT S5A (MULTI	1596.436	686.84	2.324	2	2	16
E6317		3693.232	1589.59	2.323	2	1	4
E4510		348.308	150.18	2.319	2	3	20
E6086		5361.782	2318.79	2.312	2	2	3
E285		352.491	152.61	2.31	1	2	9
E515	2708751 (AC003952) hypothetical protein [Arabidopsis t... +3 242 8.2	1528.666	661.66	2.31	1	1	10
E617		2 6114.476	2650.53	2.307	3	4	10
E4967	G262	331.419	143.85	2.304	4	1	21
E5693	2244758 (Z97335) hypothetical protein [Arabidopsis tha... +3 363 1.5	1536.211	666.79	2.304	2	2	3
E5484	4558563 (AC007138) putative NifU-like metallocluster a... +2 538 4.4	2995.213	1302.95	2.299	1	2	2
E6825		5925.147	2577.22	2.299	2	2	5
E5360	3128185 (AC004521) unknown protein [Arabidopsis thaliana] +2 257	844.798	368.09	2.295	1	1	2
E6906	3894177 (AC005312) unknown protein [Arabidopsis thaliana] +2 231	417.701	182.09	2.294	1	1	6
E6964	3928089 (AC005770) putative osr40 [Arabidopsis thaliana] +2 477 1	3306.903	1441.83	2.294	3	3	6
E5389	2160182 (AC000132) EST s gb ATTS1236.gb T43334.gb N9701... +3	3660.669	1597.13	2.292	3	3	2
E6887		915.611	401.64	2.28	1	3	6
E6888	G859	786.888	345.37	2.278	1	3	6
E4497	G643	358.633	157.61	2.275	2	3	19
E6967	4371292 (AC006260) unknown protein [Arabidopsis thaliana] +1 723	423.346	186.14	2.274	1	1	7
E6559	G1099	814.339	358.06	2.274	3	1	5
E5677	3123329 (AJ005929) squalene epoxidase homologue [Arabi... +1 369	1047.545	460.62	2.274	2	2	2
E5706	3776558 (AC005388) Identical to gb L14814 DNA for tiss... +1 627 1.	2032.895	894.3	2.273	2	2	2
E4903	G1493	368.316	162.09	2.272	4	1	20
E6934	1653655 (D90915) ATP-dependent Clp protease proteolyti... +3 184	2146.173	946.73	2.267	1	1	7
E1869	2262177 (AC002329) hypothetical protein similar to T18... +3 337 1.7	6021.645	2658.68	2.265	4	1	19
E6405	136641 UBIQUITIN-CONJUGATING ENZYME E2-20 KD (UBIQUIT... +3 3159.067	3159.067	1395.69	2.263	2	1	4
E4008	AtRanBP1b protein	544.963	241.01	2.261	1	1	1
E5449	3395938 (AF076924) polypyrimidine tract-binding protei... +3 318 5.5	1698.24	751.12	2.261	1	2	2
E3575	2052379 (U66343) calreticulin [Arabidopsis thaliana] +3 126 1.5e-	11986.21	5300.27	2.261	3	1	15
E14	128405 Putative NODULIN 21 (N-21) >pir S08632 nodulin-21 - so... +	1729.13	765.36	2.259	2	2	7
E2006	3367576 (AL031135) NAM / CUC2 -like protein [Arabidops... +1 447	1832.971	811.57	2.259	2	3	11
E5329		916.304	406.05	2.257	4	1	7
E2945	464863 26S PROTEASE REGULATORY SUBUNIT 8 (TAT-BINDING.	2038.978	905.1	2.253	1	2	13

E1491	3193289 (AF069298) similar to several small proteins (... +1 415 4.7€	1787.852	794.01	2.252	2	1	18
E5738	2702277 (AC003033) putative cyclin g-associated kinase... +1 410 6.	361.793	160.69	2.251	1	1	3
E1186	3935169 (AC004557) F17L21.12 [Arabidopsis thaliana] +1 211 7.	1755.179	780.94	2.248	4	4	16
E5491	2497538 PYRUVATE KINASE, CYTOSOLIC ISOZYME >gj 466350 ...	1176.234	523.57	2.247	3	4	2
E2285	1363482 IAA11 protein - Arabidopsis thaliana >gj 97292... +3 434 4.5	2040.626	908.6	2.246	1	2	12
E7033		683.766	304.59	2.245	1	2	7
E5942	3044214 (AF057044) acyl-CoA oxidase [Arabidopsis thali... +1 462 5	1467.037	653.51	2.245	2	3	3
E2332	4581180 (AC006220) putative glycine-rich protein [Arab... +3 117 1.8	1664.9	742.03	2.244	1	4	12
E2807		4128.102	1839.39	2.244	3	1	13
E4301	G9	326.366	145.48	2.243	1	1	19
E36		7759.504	3461.56	2.242	2	2	8
E5971	2462823 (AF000657) unknown protein [Arabidopsis thalia... +2 320 2	767.167	342.27	2.241	4	1	3
E4007	CYSTEINE PROTEINASE 2 PRECURSOR	2400.949	1071.79	2.24	2	3	1
E4113	cystatin B	1097.699	490.48	2.238	4	3	21
E441	1345592 14-3-3-LIKE PROTEIN GF14 EPSILON >gj 1022778 (... +1	4168.734	1863.4	2.237	2	2	8
E7018		2941.484	1315.48	2.236	1	2	7
E6517	2492635 ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYD	3189.958	1427.88	2.234	1	1	6
E774	2642159 (AC003000) putative mannose-1-phosphate guanyl... +1 281	15021.23	6723.23	2.234	4	3	10
E5807	4432846 (AC006283) unknown protein [Arabidopsis thaliana] +1 639	829.294	371.62	2.232	1	1	3
E6901	3881976 (AJ012409) hypothetical protein [Homo sapiens] +3 548 3	569.863	255.49	2.23	1	1	6
E4243	G738	776.563	348.16	2.23	1	2	21
E5607	3319340 (AF077407) contains similarity to E. coli cati... +3 467 1.5e-	2792.196	1252.31	2.23	4	3	2
E1267	2190551 (AC001229) Similar to C. elegans hypothetical ... +3 309 7.1	2464.681	1105.53	2.229	1	1	17
E6878		1422.257	639.01	2.226	4	2	6
E6760	2583124 (AC002387) 5-enolpyruvylshikimate-3-phosphate ... +2 444	1815.726	815.82	2.226	2	3	6
E5514	4468980 (AL035605) formamidase-like protein [Arabidops... +1 508	1977.73	890.02	2.222	1	2	2
E5809	4585983 (AC005287) Unknown protein [Arabidopsis thaliana] +3 182	1006.431	453.2	2.221	1	1	3
E6986		1142.294	514.22	2.221	1	2	6
E4155	BioB	2594.798	1168.1	2.221	4	3	22
E385		1884.916	849.48	2.219	2	1	9
E5847	1532165 (U63815) similar to dehydrogenase encoded by G... +2 506	517.021	233.19	2.217	1	4	3
E6042		941.93	425.28	2.215	2	2	3
E4004	pectinesterase	4220.655	1906.98	2.213	1	2	1
E5817	3980254 (AJ006053) peroxisomal membrane protein [Arabi... +1 778	424.714	192.22	2.21	1	1	3
E202	4508078 (AC005882) 64134 [Arabidopsis thaliana] +3 330 1.8€	3773.66	1708.4	2.209	1	2	8
E200	1402900 (X98322) peroxidase [Arabidopsis thaliana] >em... +3 248 2	1914.446	866.88	2.208	2	3	16
E5815	4191782 (AC005917) WD-40 repeat protein [Arabidopsis t... +3 586	576.275	261.15	2.207	1	1	3

E5282	1076331 histidine transport protein - Arabidopsis thal... +3 1002 3.0e-	2547.153	1154.25	2.207	2	1	7
E4767	G7	345.546	156.61	2.206	3	1	21
E3452	4490309 (AL035678) peroxidase ATP17a-like protein [Ara... +3 548	3820.164	1731.76	2.206	2	3	14
E3754	2213590 (AC000348) T7N9.10 [Arabidopsis thaliana] +2 349 8.8	3823.256	1732.84	2.206	2	4	15
E4887	G1219	759.8	344.7	2.204	4	1	20
E4891	G784	339.994	154.58	2.199	2	1	20
E6657	1755152 (U75187) germin-like protein [Arabidopsis thal... +1 829 7.9	711.69	323.74	2.198	3	2	6
E1481	2829898 (AC002311) Hypothetical protein [Arabidopsis t... +1 228 3.	4067.911	1851.82	2.197	2	1	18
E5429		6705.58	3052.56	2.197	3	3	2
E5660	120667 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, C	860.201	392.19	2.193	2	2	2
E5490		1119.084	510.78	2.191	3	4	2
E5452		9479.94	4327.76	2.19	1	2	2
E4797	G1216	507.271	231.69	2.189	1	2	21
E2939	1628622 (U72631) flavonol synthase [Arabidopsis thalia... +2 229 7.2	2528.506	1155.23	2.189	3	2	13
E6363	1922242 (Y10084) hypothetical protein [Arabidopsis tha... +1 334 1.8	7960.856	3639.86	2.187	2	3	4
E5052	G1099	348.57	159.45	2.186	2	2	21
E3225	730526 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLO	826.236	378.41	2.183	3	1	14
E1796		508.386	233.06	2.181	1	1	13
E33		3395.433	1557.08	2.181	4	4	7
E5949		646.547	297.25	2.175	2	1	4
E1029		484.788	223.23	2.172	1	2	16
E2720		3678.919	1693.7	2.172	1	2	8
E4030	4-coumarate:coa ligase - like	733.633	338.01	2.17	1	1	1
E4006	VACUOLAR ATP SYNTHASE	6174.026	2844.98	2.17	2	2	1
E4586	G1427	321.618	148.49	2.166	4	3	20
E1999		2758.036	1274.05	2.165	4	1	11
E2370	4468986 (AL035605) putative protein [Arabidopsis thali... +3 468 1.1€	6899.581	3191.45	2.162	2	1	12
E5480	4530441 (AF117756) thyroid hormone receptor-associated... +1 158	1677.852	776.94	2.16	1	2	2
E3685	121902 HISTONE H1.1 >pir HSMU11 histone H1.1 - Arabi... +3 338	3304.503	1530.32	2.159	2	3	15
E2708	4587615 (AC006951) putative acyl-CoA synthetase [Arabi... +2 264 5	1153.404	534.83	2.157	1	2	8
E274	3941480 (AF062894) putative transcription factor [Arab... -1 157 2.7e	487.331	226.28	2.154	1	2	9
E1077	1346387 KNOTTED-LIKE HOMEBOX PROTEIN 3 >emb CAA63130	6326.609	2936.83	2.154	2	3	16
E2222		1540.824	715.68	2.153	1	3	12
E2670		4356.137	2022.91	2.153	1	2	8
E6346	3763930 (AC004450) unknown protein [Arabidopsis thaliana] +1 613	1377.704	640.13	2.152	2	1	4
E6394		1367.16	635.53	2.151	2	1	5
E1438		1819.308	845.61	2.151	4	3	17

E5570	3759184 (AB018441) phi-1 [Nicotiana tabacum]	+3	212	1.5e-	699.507	325.36	2.15	2	1	2
E4014	CATALASE 3				7443.877	3463.97	2.149	4	2	1
E5789	4585983 (AC005287) Unknown protein [Arabidopsis thaliana]	+3	399		1530.296	712.31	2.148	1	1	4
E265	99725 glycine-rich protein PUTG1 - Arabidopsis thali...	+3	504	1.7e-	323.029	150.55	2.146	1	4	9
E4852	G1278				962.419	448.56	2.146	3	2	21
E2348	2702281 (AC003033) putative protein disulfide isomeras...	+2	732	1.1	1187.843	553.58	2.146	3	4	12
E4053	endochitinase				1095.189	510.61	2.145	1	4	1
E5453	4262186 (AC005508) Highly similar to cullin 3 [Arabido...	+3	740	1.7e	2019.824	943.03	2.142	1	2	2
E5371	4455349 (AL035524) putative protein [Arabidopsis thali...	+1	272	6.7e	2793.447	1305.45	2.14	1	3	2
E1335					422.408	197.63	2.137	1	4	17
E216	4584520 (AL049607) enoyl-CoA hydratase-like protein [A...	+2	410	1.	1355.736	634.35	2.137	1	2	8
E4083	13-Human lysosomal acid lipase/cholesteryl esterase				3574.403	1672.7	2.137	2	4	2
E4789	Maybe G881, Bad Sequence				395.86	185.36	2.136	1	2	20
E0	NUL				496.912	232.76	2.135	3	2	2
E6303	4468805 (AL035601) auxin-responsive GH3-like protein [...	+1	964	3.	1979.15	927.01	2.135	3	4	5
E1691	4455287 (AL035527) putative protein [Arabidopsis thali...	+1	239	1.5e	914.85	428.89	2.133	3	1	19
E2820					648.076	304.38	2.129	3	3	14
E1432	4185513 (AF102823) actin depolymerizing factor 5 [Arab...	+3	595	1.	3788.252	1781.77	2.126	2	3	17
E5184	3152614 (AC004482) unknown protein [Arabidopsis thaliana]	+2	734		1680.953	790.94	2.125	2	2	7
E2328	3193324 (AF069299) contains similarity to WD domains, ...	+1	523	6.	2321.4	1092.56	2.125	1	4	12
E5919	2062157 (AC001645) jasmonate inducible protein isolog ...	+2	321	1.	966.162	455.04	2.123	1	2	4
E6385	4455246 (AL035523) putative protein [Arabidopsis thali...	+2	694	1.3e	3677.398	1733.36	2.122	4	1	4
E6068					2065.213	973.81	2.121	4	4	3
E4349	G921				854.439	403.05	2.12	1	1	20
E6595	3399769 (U76299) uclacyanin II [Arabidopsis thaliana]	+3	645	3.5e	1030.934	486.35	2.12	3	1	6
E1256	1523800 (Y07694) MAP kinase alpha protein kinas...	+1	181	5	2115.815	998.17	2.12	1	3	18
E6000	121902 HISTONE H1.1 >pir HSMU11 histone H1.1 - Arabi...	+1	880		2371.732	1120.26	2.117	2	3	3
E5737	2129570 DAD-1 homolog - Arabidopsis thaliana >emb CAA6...	+1	340		941.018	444.76	2.116	1	1	3
E2093					1911.168	903.61	2.115	2	2	11
E2255	3292829 (AL031018) putative protein [Arabidopsis thali...	+3	172	8.3e	1965.859	930.13	2.114	3	1	12
E646					3812.053	1804.57	2.112	1	2	10
E2429	4512664 (AC006931) putative ribose phosphate pyrophosp...	+2	193		3133.306	1485.96	2.109	4	1	12
E5456					2252.928	1068.87	2.108	3	2	2
E5512					2613.674	1239.66	2.108	1	2	2
E2752	1362162 beta-glucosidase BGQ60 precursor - barley >gil...	+3	224	2.	442.17	209.82	2.107	1	1	13
E1744	3080402 (AL022603) putative NADPH quinone oxidoreducta...	+2	650		2788.994	1323.93	2.107	1	4	18
E6287	3355480 (AC004218) Medicago nodulin N21-like protein [...	+1	130	5	1012.354	480.7	2.106	3	4	4

E2994	3548819 (AC005313) putative heterogeneous nuclear ribo...	+1	120	1936.701	919.69	2.106	1	4	13
E1101	127045 S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE			1077.472	511.98	2.105	2	3	16
E1028	585350 CASEIN KINASE II, ALPHA CHAIN 2 (CK II) >pir ...	+3	113	421.419	200.39	2.103	1	4	16
E6551	2702263 (AC003033) mitochondrial F1-ATPase, gamma subu...	+3	1	1960.671	932.33	2.103	1	1	5
E3515	4559394 (AC006526) unknown protein [Arabidopsis thaliana]	+3	171	2271.956	1080.31	2.103	4	4	14
E1573	2262105 (AC002343) unknown protein [Arabidopsis thaliana]	-2	149	2891.204	1375.51	2.102	2	2	18
E669	1304227 (D63781) Epoxide hydrolase [Glycine max] >emb ...	+1	292	4952.893	2358.44	2.1	1	4	10
E888				319.885	152.54	2.097	1	3	11
E130	3738323 (AC005170) hypothetical protein [Arabidopsis t...	+3	372	670.289	320.4	2.092	1	1	9
E5736				1497.091	715.72	2.092	2	2	2
E6231	2829133 (AF043351) adenosine-5'-phosphosulfate-kinase ...	+1	869	3408.073	1630.69	2.09	1	2	4
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th...	+2	564	3954.261	1892.05	2.09	2	2	14
E5392	4417287 (AC007019) unknown protein [Arabidopsis thaliana]	+2	315	502.954	241.09	2.086	1	1	2
E2498				865.44	414.87	2.086	1	3	7
E4738	G1030			690.998	332.8	2.076	1	3	21
E5086	G376			423.886	204.79	2.07	1	1	22
E4040	cyclophilin			1515.814	733.13	2.068	3	2	1
E5500	2911148 (AB005808) NADP-malic enzyme [Aloe arborescens]	+1	15	1562.978	755.79	2.068	1	2	2
E5400	4567225 (AC007119) unknown protein [Arabidopsis thaliana]	+1	523	1855.15	897	2.068	1	1	2
E660	3183454 HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTE...			4881.54	2360.51	2.068	1	2	10
E3345	1946690 (U94495) glutathione peroxidase [Arabidopsis t...	+1	412	430.147	208.11	2.067	1	4	14
E5741	2252830 (AF013293) weak similarity to receptor protein...	+2	251	816.511	395.1	2.067	1	1	3
E2319	1170191 HOMEBOX PROTEIN HD1 >pir S47535 homeodomain-...			968.57	468.84	2.066	1	2	12
E2175	4262174 (AC005508) 9058 [Arabidopsis thaliana]	+3	433	4169.081	2017.64	2.066	1	1	11
E6353				2628.688	1272.82	2.065	4	1	4
E4007	CYSTEINE PROTEINASE 2 PRECURSOR			2687.393	1301.7	2.065	1	3	1
E5824	1617274 (Z72152) AMP-binding protein [Brassica napus]	+3	489	520.747	252.58	2.062	1	3	4
E7065	459931 (M17703) contiguous repeat polypeptide [Rattus...	+3	94	878.57	426.28	2.061	3	2	7
E5497	4097555 (U64910) ATRP7 [Arabidopsis thaliana]	+3	568	1009.304	490.49	2.058	1	2	3
E1072				6986.506	3395.26	2.058	2	1	16
E5176				5124.276	2491.21	2.057	2	2	7
E6055	3258569 (U89959) Similar to yeast general negative reg...	+1	781	801.572	389.88	2.056	2	2	3
E6495				1701.857	827.61	2.056	2	2	5
E6371	1825645 (U88173) weak similarity to Arabidopsis thalia...	+1	224	9709.859	4724.71	2.055	4	3	4
E2557				2365.547	1151.49	2.054	2	2	12
E5555				2473.02	1204.09	2.054	2	3	2
E2436	2578442 (X67426) pectinesterase [Pisum sativum]	+2	117	4513.03	2197.66	2.054	2	3	12

E4689	G664		1697.311	827.05	2.052	1	3	20
E968	585960	PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT >	1060.928	517.78	2.049	1	4	16
E5917	2062169	(AC001645) ABC transporter (PDR5-like) isolog ... +1 237	2201.92	1074.48	2.049	1	2	4
E6539	3860258	(AC005824) unknown protein [Arabidopsis thaliana] +2 377	437.008	213.4	2.048	1	1	5
E6277	2829133	(AF043351) adenosine-5'-phosphosulfate-kinase ... +3 983	4627.059	2259.86	2.047	1	2	4
E2214	4455293	(AL035528) putative protein [Arabidopsis thali... +1 279 1.2	447.485	218.67	2.046	1	3	12
E3902	3858935	(AL021636) synaptobrevin-like protein [Arabido... +1 625 2.1	630.528	308.15	2.046	1	1	16
E581			2974.149	1454.4	2.045	3	3	10
E5463			1160.147	567.76	2.043	3	4	2
E238			6595.377	3227.91	2.043	1	2	9
E4092	Empty pMen20 vector 100 ng		855.808	419.07	2.042	4	1	2
E4389	G907		359.63	176.24	2.041	1	1	20
E2541			5904.514	2892.92	2.041	2	2	11
E4303	G192		422.805	207.24	2.04	1	3	19
E4405	G427		668.354	327.56	2.04	1	2	19
E6726			1184.269	580.57	2.04	2	1	5
E4050	pathogen-inducible protein CXc750		1754.469	859.89	2.04	2	2	1
E4227			359.106	176.12	2.039	3	4	22
E4694	G728		440.801	216.3	2.038	3	3	20
E0	NUL		620.549	304.54	2.038	3	1	22
E6788	2911057	(AL021961) caffeoyl-CoA O-methyltransferase - ... +2 516	2353.727	1155.76	2.037	4	3	6
E3426	2864622	(AL021811) putative protein [Arabidopsis thali... +1 342 4.8	9064.79	4450.2	2.037	2	3	14
E3066	4185139	(AC005724) putative diacylglycerol kinase [Ara... +1 499 5.5	1491.582	733.01	2.035	2	3	13
E6742	3378056	(AF017777) helicase [Drosophila melanogaster] +2 138 7	917.182	451.07	2.033	2	1	5
E5396	4510345	(AC006921) unknown protein [Arabidopsis thaliana] +3 534	2905.466	1430.82	2.031	3	1	2
E6441	114815	IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B AN.	983.652	484.82	2.029	2	2	4
E2262	G176		1057.084	520.94	2.029	1	3	12
E5408			821.445	405.54	2.026	1	1	3
E6886			941.178	464.46	2.026	1	1	6
E5944	3241945	(AC004625) unknown protein [Arabidopsis thaliana] +1 430	1905.203	941.08	2.024	2	3	3
E2046			1161.693	574.11	2.023	2	3	11
E5895			1900.649	939.83	2.022	1	2	3
E2010	3157937	(AC002131) Identical to aspartic proteinase cD... +3 118 1.5	1648.787	815.64	2.021	2	3	11
E3466			20921.95	10359.6	2.02	2	3	14
E0	NUL		384.547	190.65	2.017	4	2	22
E4032	ACYL CARRIER PROTEIN		784.04	388.65	2.017	1	1	1
E6285			1625.991	806.61	2.016	3	2	4

E2977	3341679 (AC003672) dynamin-like protein phragmoplastin... +1 269	1837.035	912.39	2.013	1	2	13
E536	465820 HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMO...	2601.127	1292.37	2.013	1	1	9
E6922	3643607 (AC005395) unknown protein [Arabidopsis thaliana] +2 342	881.654	438.13	2.012	1	1	7
E4884		649.597	322.95	2.011	4	1	20
E6333	4557647 heat shock factor binding protein 1 >gj 328340... +1 166 1.1	1617.72	804.37	2.011	2	1	5
E4743	G1552	1453.671	724.01	2.008	3	1	21
E3359	4468807 (AL035601) cytochrome P450 monooxygenase-like ... +2 75	5011.505	2495.75	2.008	1	4	14
E617		6090.818	3032.59	2.008	4	3	16
E28		17559.94	8747.12	2.008	4	2	7
E6170		642.297	320.04	2.007	1	1	5
E5768	2832679 (AL021712) putative protein [Arabidopsis thali... +3 276 1.7€	1103.394	549.7	2.007	1	1	3
E3114	4262250 (AC006200) putative aldolase [Arabidopsis thal... +3 112 4.:	3310.079	1649.37	2.007	2	3	13
E5600	4006826 (AC005970) unknown protein [Arabidopsis thaliana] +2 288	1254.524	625.48	2.006	4	1	2
E6453		1511.049	753.37	2.006	2	2	5
E484	4335749 (AC006284) unknown protein [Arabidopsis thaliana] +3 327	1668.474	831.82	2.006	4	4	9
E4390		1310.424	653.83	2.004	1	3	20
E5967	3874563 (Z81042) similar to Yeast hypothetical protein... +3 228 2.4€	663.817	331.34	2.003	2	1	3
E3310	548852 40S RIBOSOMAL PROTEIN S21 >pir S38357 ribosom... +1	1143.291	570.93	2.003	1	2	14
E5923	1707015 (U78721) protein phosphatase 2C isolog [Arabid... +1 425 4	1303.799	650.89	2.003	3	2	4
E2425		2795.373	1395.32	2.003	2	1	12
E1814		2205.072	1102.8	2	2	3	19
E896	4586044 (AC007020) putative receptor protein kinase [A... -2 185 1.1	599.156	299.75	1.999	1	3	11
E6457	3759184 (AB018441) phi-1 [Nicotiana tabacum] +3 488 5.3e-	1911.962	956.41	1.999	2	2	5
E5689		5586.2	2794.89	1.999	2	2	3
E3133	3779218 (AF030879) protein kinase CPK1 [Solanum tubero... +3 231	2148.353	1075.93	1.997	2	1	13
E3809		2941.223	1473.68	1.996	2	2	15
E6249		3892.835	1949.95	1.996	1	2	4
E6731		2451.593	1229.03	1.995	2	1	5
E2869	1170714 SHAGGY RELATED PROTEIN KINASE ASK-GAMMA >pir ..	1156.15	579.96	1.993	2	1	7
E5417		2575.543	1292.89	1.992	1	3	2
E4006	VACUOLAR ATP SYNTHASE	1576.015	792	1.99	2	1	1
E6361		1947.905	979.12	1.989	2	1	4
E6549	3599415 (AF083190) SPF31 [Homo sapiens] +1 181 2.9e	855.284	430.27	1.988	1	1	5
E2761	4093155 (AF088281) phytochrome-associated protein 1 [A... +1 662	2721.046	1368.53	1.988	3	3	13
E4055	LOW-TEMPERATURE-INDUCED 78 KD PROTEIN	912.772	459.58	1.986	1	4	1
E934		1885.381	949.39	1.986	1	3	11
E1902	4678928 (AL049711) putative serine/threonine protein k... +1 791 6.8	792.667	399.29	1.985	1	4	11

E4092	Empty pMen20 vector 100 ng	358.591	180.75	1.984	3	2	2
E4779		470.323	237.32	1.982	1	2	20
E6043	123045 PUTATIVE UROPORPHYRIN-III C-METHYLTRANSFERASE	488.1	246.41	1.981	2	2	3
E2163	4538941 (AL049483) NPR1 like protein [Arabidopsis thal... +1 580 1.	890.796	449.96	1.98	2	2	11
E5849	3386546 (AF079503) H-protein promoter binding factor-2... +2 359 3.	862.288	435.64	1.979	1	2	3
E2318		1338.745	676.56	1.979	1	4	12
E2982	2584721 (Y10157) sulfite reductase [Arabidopsis thaliana] +1 497 2.5	1836.84	929.71	1.976	1	4	13
E6821	4539419 (AL049171) putative ribosomal protein [Arabido... +2 489 2.	3081.901	1559.51	1.976	2	2	5
E2662	2497486 URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE K	6489.163	3289.58	1.973	3	2	8
E3322	4220446 (AC006216) Strong similarity to gjl2062155 T02... +3 382 1.	4269.981	2165.23	1.972	1	2	14
E5596		1928.886	978.7	1.971	2	1	2
E460	4678926 (AL049711) hypothetical protein [Arabidopsis t... +2 451 7.2	421.064	213.94	1.968	4	4	9
E5813	1709535 DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (2638.658	1341.08	1.968	3	1	3
E6288	Bad Sequence	1293.052	657.82	1.966	3	4	5
E4344	G763	1209.676	615.47	1.965	3	1	20
E6282		1801.844	916.86	1.965	1	2	5
E5982	3582340 (AC005496) unknown protein [Arabidopsis thaliana] +3 153	3024.548	1540.16	1.964	2	3	4
E2091		2121.18	1080.66	1.963	2	2	11
E4055	LOW-TEMPERATURE-INDUCED 78 KD PROTEIN	4790.686	2440.1	1.963	1	3	1
E6791		3821.22	1947.58	1.962	2	2	5
E1577	1755178 (U75200) germin-like protein [Arabidopsis thal... +3 433 5.8	1193.276	608.71	1.96	2	2	18
E6377	3687243 (AC005169) putative ribosomal protein [Arabido... +3 250 2.	3521.03	1797.14	1.959	2	1	4
E5284	1429207 (X99224) annexin [Arabidopsis thaliana] +1 597 1.5e-	2692.116	1375.11	1.958	4	1	7
E3570		7213.468	3684.2	1.958	1	1	15
E491		2441.049	1247.38	1.957	1	1	9
E1480	137465 VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SU.	1428.112	730.3	1.956	2	3	18
E1360	3879734 (Z93388) predicted using Genefinder; cDNA EST ... +1 130	2015.861	1030.98	1.955	1	2	17
E162	4455365 (AL035524) putative protein [Arabidopsis thali... +1 395 6.2e	2791.081	1427.76	1.955	3	1	8
E4459	G12	410.706	210.14	1.954	1	2	20
E4095	Human SPARC/osteonectin	29618.11	15163.06	1.953	2	3	21
E4520	G1052	413.789	212.01	1.952	4	1	20
E1673	4107099 (AB015141) AHP1 [Arabidopsis thaliana] >dbj BA... +1 488	362.199	185.85	1.949	1	1	19
E1911	4678364 (AL049659) putative protein [Arabidopsis thali... +3 301 5.7e	1968.791	1010.09	1.949	1	2	11
E4844	G1006	552.88	283.83	1.948	1	2	21
E5769	4585983 (AC005287) Unknown protein [Arabidopsis thaliana] +2 379	1004.986	516.19	1.947	1	1	3
E6902		503.967	258.95	1.946	1	1	6
E5522	1168529 SERINE/THREONINE-PROTEIN KINASE ASK1 >pir S36... +	3084.884	1585.03	1.946	1	2	2

E3065	4585976 (AC005287) Unknown protein [Arabidopsis thaliana] +2	298	4173.736	2145.18	1.946	2	1	13
E4855	G1383		421.681	216.96	1.944	3	2	21
E5424			807.85	415.93	1.942	1	1	2
E1156	4262181 (AC005508) 37496 [Arabidopsis thaliana]	+3 586 3.6€	1471.177	757.51	1.942	4	4	16
E694			4546.007	2341.36	1.942	2	1	10
E4112	cystatin B		373.124	192.19	1.941	4	1	21
E6671			1085.481	559.37	1.941	1	2	5
E5186	4678949 (AL049711) dihydrolipoamide S-acetyltransferase...	+2 565 6	4219.827	2174.03	1.941	2	2	7
E2555	2132388 PHO85 protein - yeast (Saccharomyces cerevisiae)...	+3 234	5119.299	2637.01	1.941	2	2	12
E2949	2245016 (Z97341) hypothetical protein [Arabidopsis thaliana]...	+2 360 3.2	492.865	254.14	1.939	3	2	13
E6702	82287 ubiquitin - potato (fragment) >emb CAA77738 (... +2	77 1.3€	936.801	483.09	1.939	2	1	5
E4764	G10		343.019	177.01	1.938	1	3	21
E5240	2627238 (D50565) NADH dehydrogenase subunit 5 [Oryza sativa]...	+2 35	2149.924	1109.14	1.938	2	2	7
E4055	LOW-TEMPERATURE-INDUCED 78 KD PROTEIN		2080.962	1074.52	1.937	2	3	1
E5504	3122671 HYPOTHETICAL RAE1-LIKE PROTEIN >pir S71241 pr... +2		1515.696	783.57	1.934	3	2	2
E2298			2208.173	1142.14	1.933	1	4	12
E4692	G727		1325.995	686.62	1.931	3	1	20
E3378	421941 GTP-binding protein, ras-related - common tobacco...	+3 226 4.	1501.324	777.38	1.931	3	2	14
E600			6670.229	3459.36	1.928	1	2	10
E4359			448.127	232.54	1.927	3	3	20
E194			1261.976	654.76	1.927	1	1	9
E6246	3892056 (AC002330) putative vacuolar ATPase [Arabidopsis]...	+2 625	2481.318	1287.78	1.927	1	2	4
E4603	G451		719.286	373.41	1.926	2	2	20
E4671	G566		450.51	234.07	1.925	2	2	20
E1949	4539301 (AL049480) putative mitochondrial protein [Arabidopsis]...	+2 280 6.€	1012.295	525.86	1.925	1	2	11
E406	3450842 (AF080436) mitogen activated protein kinase kinase...	+1 156 1.	1555.897	809.27	1.923	2	4	8
E3384	1351359 UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.€		2371.673	1233.21	1.923	1	2	14
E4133	A.thaliana cyclophilin		619.789	322.41	1.922	4	3	22
E5764	1709535 DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B...		2193.699	1141.3	1.922	3	1	3
E5367	4704730 (AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]...	+2 190 ;	2900.126	1508.78	1.922	3	3	2
E2644	3319353 (AF077407) contains similarity to copper-binding...	+1 578 2.0€	893.677	465.45	1.92	1	2	7
E5926			2287.164	1192.04	1.919	2	3	3
E6638	4454472 (AC006234) unknown protein [Arabidopsis thaliana]...	+1 605	2905.499	1514.32	1.919	3	2	6
E661			1823.28	950.8	1.918	1	4	10
E1957			4866.036	2537.16	1.918	1	2	11
E6383	4455246 (AL035523) putative protein [Arabidopsis thaliana]...	+3 676 1.5€	2764.17	1443.68	1.915	4	3	4
E6189	81286 extensin - Volvox carterii (fragment) >emb CAA4... +1	251 7.€	740.13	386.99	1.913	1	1	4

EXHIBIT D

EID	COMMENT	(0.868)CY3CY5	(0.868)CY3METAROWMETACOL
E840	4454029 (AL035394) tyrosine transaminase like protein ... +3 396 4.8e-36	5188.907	445.43
E986	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ23... +2	6776.597	986.01
E436		4020.197	612.22
E281	2746341 (AF037590) ATA27 [Arabidopsis thaliana] +3 330 1.2e-28	20118.45	3072.05
E2230	1076442 beta-glucosidase (EC 3.2.1.21) - rape >emb CAA... +2 428 2.0e-	17319.73	3152.38
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th... +2 564 7.6e-54	9471.079	1857.32
E3518	3668173 (AB006777) vegetative storage protein [Arabido... +1 682 1.4e-6	10372.01	2078.74
E2202		6337.206	1408.07
E1783	4589123 (AF126374) At14a protein [Arabidopsis thaliana] +1 566 4.7e-54	2418.7	559.1
E6978	3319350 (AF077407) No definition line found [Arabidops... +2 553 1.1e-52	7526.917	1841.41
E4131	A.thaliana cyclophilin	7765.349	1912.81
E808	2832649 (AL021710) adenylosuccinate lyase - like prote... +2 250 1.4e-28	16343.36	4124.77
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th... +2 564 7.6e-54	7289.709	1949.31
E5356	3319350 (AF077407) No definition line found [Arabidops... +3 894 8.1e-89	4843.083	1300.34
E2228	3413711 (AC004747) putative antifungal protein [Arabid... +3 285 2.8e-24	16292.93	4415.86
E1759		5466.373	1489.1
E1753	4388726 (AC006413) putative 12-oxophytodienoate-10,11-... +1 528 7.6e-	3016.276	832.96
E3490	2146733 GAST1 protein homolog (clone GASA1) - Arabidop... +2 537 5.5	13064.97	3613.48
E6413	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ23... +1 4010.512		1110.75
E3362	4218987 (AF098630) putative cell wall-plasma membrane ... +3 283 4.6e-	9998.805	2807.89
E6578	2244888 (Z97338) similarity to cytochrome P450 [Arabid... +2 290 4.6e-31	2028.531	570.8
E3397	4580920 (AF113545) vacuole-associated annexin VCaB42 [... +1 398 5.8e	9304.893	2630.92
E6937	3319350 (AF077407) No definition line found [Arabidops... +3 539 3.4e-51	7137.625	2026.47
E3334	3319347 (AF077407) No definition line found [Arabidops... +2 447 3.4e-66	6959.168	2081.01
E1220	2894563 (AL021890) putative protein [Arabidopsis thali... +1 293 2.7e-37	5280.938	1640.96
E1594	4559366 (AC006585) putative tyrosine transaminase [Ara... +2 335 2.1e-3	3011.26	937.67
E157	2460203 (AF021244) coronatine-induced protein 1 [Arabi... +2 247 3.0e-2	2798.22	916.87
E4540	G1356	1315.128	431.09
E540	4587542 (AC006577) Belongs to the PF100657 Lipase/Acy/... +3 372 1.7e	7077.355	2394.62
E2698	629602 probable imbibition protein - wild cabbage >em... +1 256 4.2e-20	14461.7	4898.26
E2396	1076261 beta-fructofuranosidase (EC 3.2.1.26) - red go... +2 231 5.2e-39	7588.549	2573.92
E2649	3785997 (AC005499) putative annexin [Arabidopsis thali... +1 595 1.4e-61	3894.893	1340.03
E2167	4455154 (AL033545) extensin - like protein [Arabidopsi... +2 394 2.7e-50	2498.538	872.22
E5708	3885331 (AC005623) putative cytochrome p450 protein [A... +2 269 5.6e-	4305.89	1515.78

E2546	3080393 (AL022603) NADH dehydrogenase like protein [Ar... +3 680 3.9e	8984.748	3163.28	2.84	2	4
E861	4220464 (AC006216) Similar to gb Y09437 myrosinase bin... +1 438 9.7e-	2866.318	1024.66	2.797	2	2
E741	3914996 PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT	11475.71	4135.65	2.775	2	3
E1070	1362093 hypothetical protein (clone TPP15) - tomato (f... +3 471 5.5e-44	4065.957	1487.18	2.734	4	1
E5048		4228.116	1579.74	2.676	4	2
E4767	G7	518.614	199.18	2.604	3	1
E2678	1181531 (L41244) thionin [Arabidopsis thaliana] >prf ... +2 430 7.9e-49 3	6683.22	2619.5	2.551	3	2
E2153		2943.77	1156.26	2.546	2	2
E4561	3738091 (AC005617) similar to symbiotic ammonium trans... +3 393 1.0e-	1633.45	643.3	2.539	4	1
E2477	4510339 (AC006921) putative ABC transporter protein [A... +1 621 8.4e-9	9503.943	3749.84	2.534	3	1
E4805	G1252	1093.479	432.54	2.528	1	2
E1523		3351.798	1327.63	2.525	4	2
E4186	A.thaliana type I chlorophyll a/b binding protein	608.094	243.96	2.493	4	1
E3920	4115377 (AC005967) unknown protein [Arabidopsis thaliana] +1 263 1.4e	3075.096	1236.49	2.487	3	1
E3115		18119.63	7293.75	2.484	4	1
E2513	1170121 GLUTATHIONE S-TRANSFERASE 103-1A >pir S66354 ... +2 6	6377.785	2575.39	2.476	3	1
E4408	G350	892.737	364.7	2.448	3	4
E790	4734007 (AC007178) hypothetical protein [Arabidopsis t... +3 340 4.0e-40	3976.277	1646.24	2.415	2	4
E2444	2578440 (X67425) pectinesterase [Pisum sativum] +1 147 2.6e-18	12006.51	4973.28	2.414	4	3
E4357	G921	1262.46	523.19	2.413	3	1
E6269	2118045 beta-fructofuranosidase (EC 3.2.1.26) - Arabid... +2 929 3.2e-97	3010.973	1254.43	2.4	3	2
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	3033.996	1264.86	2.399	2	2
E3753	2062156 (AC001645) jasmonate inducible protein isolog ... +2 580 1.6e-55	4825.753	2020.85	2.388	2	2
E6415	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ23... +1 3337.514	3337.514	1409.34	2.368	4	4
E4407	G353	576.462	244.81	2.355	3	2
E6340		1863.802	794.61	2.346	4	3
E1918		4466.357	1912.12	2.336	3	4
E1693	4468807 (AL035601) cytochrome P450 monooxygenase-like ... +3 269 4.2 5711.192	2458.17	2458.17	2.323	1	2
E1654	1762933 (U66263) tumor-related protein [Nicotiana taba... +3 178 1.5e-25	8887.31	3840.28	2.314	3	3
E4710	G1241	9089.632	3931.25	2.312	3	3
E2542	3434969 (AB008104) ethylene responsive element binding... +2 422 2.2e-	12955.5	5626.32	2.303	2	4
E132		3047.595	1328.46	2.294	1	1
E2137	3164222 (AB008518) RMA1 [Arabidopsis thaliana] >gi 420... +1 413 7.6e-	11335.91	4950.95	2.29	2	2
E2331	4539330 (AL0356679) putative receptor-like protein kina... +1 261 6.5e-21	3547.126	1559.21	2.275	1	2
E1761	602292 (U17987) RCH2 protein [Brassica napus] +1 317 4.1e-33	4394.554	1941.1	2.264	3	2

E5076	G28	1789.691	790.78	2.263	3	3
E234	4468813 (AL035601) putative protein [Arabidopsis thaliana]	6624.348	2926.98	2.263	3	2
E3693		2692.147	1192.57	2.257	4	3
E3389	399298 STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6... +2	3794.505	1690.87	2.244	3	4
E2429	4512664 (AC006931) putative ribose phosphate pyrophosph... +2	1878.59	838.09	2.242	4	1
E4015	jasmonate inducible protein	2598.641	1161.74	2.237	4	3
E3354	2500376 60S RIBOSOMAL PROTEIN L34 >gb AAD14494 (AC005... +1	5697.628	2577.14	2.211	3	2
E4014	CATALASE 3	2928.505	1326.95	2.207	4	2
E5447	4056465 (AC005990) F5O8.40 [Arabidopsis thaliana]	1785.014	814.18	2.192	3	3
E1033	3201632 (AC004669) putative 2A6 protein [Arabidopsis t... +1	4405.836	2034.41	2.166	3	2
E583	4263704 (AC006223) putative sugar starvation-induced p... +1	3732.022	1724.33	2.164	3	3
E4015	jasmonate inducible protein	2582.551	1195.04	2.161	4	4
E4026	thionin	1756.298	816.69	2.151	1	1
E4026	thionin	1403.992	654.86	2.144	2	2
E4015	jasmonate inducible protein	3223.492	1508.52	2.137	3	4
E175	3192102 (AB013397) polygalacturonase inhibitor [Citrus... +2	1967.905	922.53	2.133	3	3
E3608	3157947 (AC002131) Similar to protein gb Z74962 from B... +2	16764.23	7899.69	2.122	3	2
E2374	2290532 (U94748) AN11 [Petunia x hybrida]	842.812	398.51	2.115	4	1
E5935		3008.656	1427.79	2.107	2	1
E4585	G1426	639.743	306.85	2.085	4	1
E4532	G1314	548.562	263.78	2.08	4	1
E1587	3540183 (AC004122) Highly Similar to branched-chain am... +1	4418.124	2136.84	2.068	2	2
E5134	2117612 catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana	4856.161	2359.52	2.058	3	3
E2267		1504.016	733.68	2.05	3	1
E4662	G545	2620.197	1293.62	2.025	4	4
E2211	3281848 (AL031004) putative protein [Arabidopsis thaliana]	7075.941	3497.36	2.023	1	1
E3047		11457.88	5680.62	2.017	2	2
E4835	G1447	773.169	383.98	2.014	3	2
E1340	3927837 (AC005727) putative core protein [Arabidopsis ... +3	2357.822	1175.7	2.005	3	2
E1312	3738340 (AC005170) GMP synthase-like protein [Arabidop... +2	3579.4	1789.57	2	1	2
E1477	1170034 GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GL... +2	6117.024	3075.55	1.989	2	1
E4005	3' flavonoid O-methyltransferase	1857.398	934.4	1.988	2	3
E2628	1946364 (U93215) lipase isolog [Arabidopsis thaliana]	9675.44	4872.79	1.986	4	2
E4349	G921	2167.164	1095.74	1.978	1	1
E2478	4432856 (AC006300) putative 2A6 protein [Arabidopsis t... +1	6334.342	3208.95	1.974	3	3

E4451	G268					848.765	457.01	1.857	3	2
E3821						2995.301	1617.51	1.852	2	2
E772	2460188 (AF020785)	polygalacturonase inhibiting protei...	+3	316	7.7e-32	4895.1	2649.12	1.848	4	3
E4560	G787					1351.498	732.48	1.845	4	3
E2950						1475.118	803.5	1.836	3	4
E3644	3377751 (AF079511)	glutathione S-transferase [Mesembry...	+3	229	5.0e-	11179.72	6089.08	1.836	3	2
E3851	3894183 (AC005662)	calmodulin-like protein [Arabidopsi...	+3	462	3.2e-46	5308.422	2894.45	1.834	3	3
E4026	thionin					1116.589	609.19	1.833	2	1
E2472						3188.745	1739.72	1.833	1	3
E3077	2160189 (AC000132)	Similar to A. thaliana receptor-lik...	+2	130	2.1e-05	3118.331	1702.88	1.831	2	1
E2589	2655098 (AF023472)	peptide transporter [Hordeum vulgare]	+3	366	1.8e-	5722.994	3129.79	1.829	2	4
E2578	4455220 (AL035440)	putative aconitase [Arabidopsis tha...	+3	194	2.4e-13	11252.28	6163.96	1.825	2	2
E2143						2571.513	1414.8	1.818	4	2
E5182	2062161 (AC001645)	jasmonate inducible protein isolog ...	+1	687	7.0e-67	7887.971	4341.74	1.817	4	2
E3530	3695019 (AF055848)	subtilisin-like protease [Arabidops...	+1	349	6.3e-33	3722.771	2050.03	1.816	2	4
E1895	3342798 (AF061240)	glutamine cyclotransferase precurs...	+1	446	2.4e-4	2408.355	1332.77	1.807	3	2
E5660	120667 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTO					2015.444	1117.19	1.804	2	2
E4014	CATALASE 3					3527.322	1954.92	1.804	4	1
E1493	2062164 (AC001645)	jasmonate inducible protein isolog ...	+1	555	6.9e-53	11201.44	6212.48	1.803	2	1
E4040	cyclophilin					2725.003	1514.09	1.8	4	2
E4324	G501					1520.548	845.98	1.797	3	1
E4526	G1125					2118.341	1178.89	1.797	2	3
E6095	2062157 (AC001645)	jasmonate inducible protein isolog ...	+2	517	2.2e-70	2344.823	1305.21	1.797	2	4
E3666						5587.823	3114.08	1.794	3	2
E5430	CATALASE 3					3935.49	2194.96	1.793	3	1
E4014	4469007 (AL035602)	UDP rhamnose-anthocyanidin-3-glucos...	+2	674	4.2	3614.989	2227.82	1.79	3	1
E3686						3988.391	2021.18	1.789	2	1
E4023	GAST1 protein					6308.082	3525.66	1.789	4	4
E4056	PUTATIVE TRYPSIN INHIBITOR T01024.25 PRECURSOR					2038.259	1139.91	1.788	2	1
E1607	2660677 (AC002342)	unknown protein [Arabidopsis thaliana]	+2	663	2.5e	3741.846	2102.77	1.779	3	1
E1431	2342687 (AC000106)	Similar to Beta integral membrane p...	+3	510	4.0e-4	3856.614	2167.27	1.779	2	1
E4299	G184					816.161	459.13	1.778	3	4
E4458	G179					621.181	349.73	1.776	3	4
E3585	2129769	xyloglucan endo-transglycosylase precursor - A...	+1	756	3.5e-74	29388.52	16548.88	1.776	3	1
E4943	G791					819.25	462.83	1.77	4	1

E4126	prohibitin	1005.7	568.86	1.768	2	1
E1078	231683 CALNEXIN HOMOLOG PRECURSOR >pir JN0597 calnex... +3 1	18022.91	10196.11	1.768	4	1
E1571	4455186 (AL035521) putative protein [Arabidopsis thali... +3 176 9.5e-16	1189.052	672.98	1.767	4	2
E746		1764.125	998.27	1.767	4	3
E2290		5826.125	3296.42	1.767	3	4
E7049	4103952 (AF029980) A37 [Arabidopsis thaliana] >gj 4103... +1 713 1.2e-7	1752.531	995.53	1.76	3	2
E1043	2688839 (AF003347) ATP phosphoribosyltransferase [Thla... +3 215 2.4e	864.871	491.94	1.758	3	2
E5284	1429207 (X99224) annexin [Arabidopsis thaliana] +1 597 1.5e-78 3 3331.951	7901.031	1897.35	1.756	4	1
E499		659.807	4498.7	1.756	3	1
E4522		3752.85	376.14	1.754	4	3
E3146	3786011 (AC005499) putative elongation factor [Arabido... +3 688 5.2e-72	723.435	2145.54	1.749	1	3
E0	NUL		414.13	1.747	2	4
E5245	4126403 (AB011796) flavonol synthase [Citrus unshiu] +3 226 1.4e-21	1811.057	1039.14	1.743	2	2
E2693	1362021 zink finger protein 7 - Arabidopsis thaliana >... +1 645 2.0e-62 1 1992.247	1144.62	1144.62	1.741	1	4
E1208	1351082 SUPEROXIDE DISMUTASE, CHLOROPLAST PRECURSOR (F... 3432.088	1971.4	2682.36	1.741	2	4
E1458	1708924 MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NAD... +2 4669.477	1038.703	597.29	1.739	1	3
E6635	2829898 (AC002311) Hypothetical protein [Arabidopsis t... +2 594 5.1e-57	1905.831	1095.66	1.739	4	4
E415	3341687 (AC003672) putative ras protein [Arabidopsis t... +1 153 2.7e-10	1176.217	677.22	1.737	3	2
E985	1174870 UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 K... 2925.824	1684.84	1684.84	1.737	2	4
E4005	3' flavonoid O-methyltransferase	1163.764	670.4	1.736	3	1
E4356	G993	1797.25	1036.63	1.734	2	4
E828	2213610 (AC000103) F21J9.4 [Arabidopsis thaliana] +1 149 6.1e-13	4047.854	2334.37	1.734	2	3
E1840	1171991 PHENYLALANINE AMMONIA-LYASE 1 >pir S52990 phe... +1 9	19603.35	11309.38	1.733	3	2
E3664	2338712 (AF013959) metallothionein-like protein [Arabi... +1 384 9.0e-35	3502.268	2022.5	1.732	1	2
E1909	3402676 (AC004697) putative myrosinase-binding protein... +2 707 5.4e-6	5863.432	3386.03	1.732	2	4
E2104	G346	540.925	312.75	1.73	2	1
E4947	G284	1345.371	777.51	1.73	3	2
E4471	2660677 (AC002342) unknown protein [Arabidopsis thaliana] +3 436 2.8e	2284.076	1320.55	1.73	4	2
E6114	G1427	770.844	446.23	1.727	4	3
E4586	1628622 (U72631) flavonol synthase [Arabidopsis thalia... +1 114 2.6e-06	5075.727	2938.45	1.727	3	1
E2535	2739389 (AC002505) Cf-2.2 like protein [Arabidopsis th... +2 191 2.2e-27	6791.211	3934.34	1.726	4	2
E483	2960364 (AJ224986) cinnamoyl CoA reductase [Populus ba... +1 224 6.2e	1488.473	862.74	1.725	3	2
E996	glutamate--ammonia ligase	2575.973	1498.05	1.72	2	3
E4057	4467097 (AL035538) heat shock protein 70 like protein ... +3 584 5.8e-56	22562.47	13116.06	1.72	2	4
E2623						

E717	3860163 (AF098962) disease resistance protein RPP1-WsA... +2 160 1.4	3477.813	2024.43	1.718	2	3
E1690	2271485 (AF009647) arginine decarboxylase [Arabidopsis... +3 552 1.4e-	4356.231	2536.52	1.717	3	3
E4010	thioredoxin	4332.748	2527.22	1.714	2	2
E4844	G1006	1176.85	688.53	1.709	1	2
E1295	452470 (U05218) ATP sulfurylase [Arabidopsis thaliana] +2 727 4.0e-71	8355.201	4891.51	1.708	3	1
E4542	G1363	583.604	342.29	1.705	2	3
E5665		2090.189	1225.58	1.705	4	2
E4452	G194	840.139	493.22	1.703	3	2
E2493		3246.741	1908.09	1.702	1	1
E6885	3080371 (AL022580) putative pectinacetyltransferase prote... +2 459 9.6e-49	5991.105	3523.77	1.7	2	2
E4345	G867	2653.929	1562.07	1.699	3	1
E774	2642159 (AC003000) putative mannose-1-phosphate guanyl... +1 281 1.7	12651.5	7456.91	1.697	4	3
E4852	G1278	1010.534	595.94	1.696	3	2
E4045	Myrosinase	3113.983	1837.59	1.695	4	3
E3683	1170505 EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >... +3 664	2650.805	1565.94	1.693	2	3
E3769	4218535 (AJ010829) GRAB1 protein [Triticum sp.] +2 493 2.6e-46	3804.224	2251.04	1.69	4	2
E6788	2911057 (AL021961) caffeoyl-CoA O-methyltransferase - ... +2 516 9.4e-4	1703.639	1008.79	1.689	4	3
E44		12770.44	7566.2	1.688	4	2
E1928	3127890 (AJ006024) cysteine synthase, O-acetyl-L-serin... +2 182 2.9e-2	4236.586	2516.12	1.684	3	4
E4503	G859	1403.896	834.07	1.683	4	1
E5475	3786008 (AC005499) unknown protein [Arabidopsis thaliana] +1 175 4.0e	508.165	302.15	1.682	3	4
E4559	G780	899.488	534.9	1.682	4	1
E3497	3935167 (AC004557) F17L21.10 [Arabidopsis thaliana] +1 425 4.1e-3	4587.877	2731.62	1.68	4	2
E3744	282865 chlorophyll a/b-binding protein - Arabidopsis ... +3 600 1.6e-66	5548.433	3302.98	1.68	2	3
E3777		5483.347	3270.13	1.677	2	2
E4794	G915	1144.316	682.61	1.676	3	4
E5677	3123329 (AJ005929) squalene epoxidase homologue [Arabi... +1 369 9.7e	1241.919	741.45	1.675	2	2
E6301	3915639 ALTERNATIVE OXIDASE 1A PRECURSOR >dbj BAA22625... +1	2274.738	1362.67	1.669	3	2
E3925	1351272 TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi... +3	2311.039	1386.63	1.667	3	3
E3641		4923.668	2959.48	1.664	3	4
E1581	2245055 (Z97342) resistance gene homolog (fragment) [A... +3 519 1.9e-5	1517.207	912.06	1.663	4	2
E3555		7171.825	4311.83	1.663	3	3
E1088	3402716 (AC004261) unknown protein [Arabidopsis thaliana] +1 204 1.8e	15446.4	9288.54	1.663	4	1
E725	2129648 MYB-related protein 33,3K - Arabidopsis thalia... +3 362 8.6e-62	4013.888	2420.4	1.658	4	3
E1525	2160152 (AC000375) ESTs gb U75592.gb T13956.gb T43869 ... +2 452 1	925.974	559.9	1.654	2	2

E1862		2954.498	7420.57	2.512	L28P1A01,L35P119E08
E3403	3913418 S-ADENOSYLMETHIONINE DECARBOXYLASE PROI	4660.478	11698.55	2.51	L15P8E06,L35P103A02
E3783	2677828 (U93166) cysteine protease [Prunus armeniaca]	2601.66	6528.26	2.509	L17P1D10,L35P108F03
E2892		2471.941	6202.71	2.509	L16P2F08,L35P79D12
E1143		511.656	1283.66	2.509	L17P8H01,L35P112D01
E1446	3766368 (AL031907) putative trascription factor, ccr4-...	1376.995	3453.15	2.508	L20P15H07,L35P115G06
E749	4455274 (AL035527) spliceosome associated protein-like...	558.716	1398.59	2.503	L18P10D08,L35P87D11
E3829	4507433 testis enhanced gene transcript >sp P55061 TEG... +3	8159.658	20413.37	2.502	L17P1G02,L35P108F09
E3718	3738285 (AC005309) unknown protein [Arabidopsis thaliana] +3	3299.244	8238.93	2.497	L17P14D03,L35P107A07
E3863	4678328 (AL049658) aldehyde dehydrogenase (NAD+)-like ... +1	1359.493	3393.39	2.496	L17P23E05,L35P109D04
E1495	4455208 (AL035440) putative protein [Arabidopsis thali... +1 49	925.96	2311.16	2.496	L20P17D01,L35P115H07
E2832	4538928 (AL049483) putative protein [Arabidopsis thali... +1 16	733.718	1828.75	2.492	L16P1G11,L35P79B06
E2252		628.026	1559.89	2.484	L22P11D02,L35P93F08
E2254	G1181	1112.733	2761.1	2.481	L22P11D07,L35P93F10
E1467	G583	1415.528	3507.02	2.478	L20P10B06,L35P115C09
E3555		1371.352	3395.8	2.476	L16P5F07,L35P105F02
E4663	G525	568.188	1405.36	2.473	J124F07F1
E2171		571.767	1413.42	2.472	L20P7E03,L35P92H11
E1330	1710585 60S ACIDIC RIBOSOMAL PROTEIN P0 >emb CAA637	3130.718	7734.15	2.47	L18P34B06,L35P114D03
E3747	1173221 40S RIBOSOMAL PROTEIN S11-BETA >gij 166869 (LC	1375.64	3397.65	2.47	L17P17F05,L35P107H07
E3732	3096939 (AL023094) putative protein [Arabidopsis thali... +2 48	3591.088	8859.4	2.467	L17P15H06,L35P107C09
E1681	4262173 (AC005508) 3975 [Arabidopsis thaliana] +3 21	1462.24	3606.09	2.466	L22P24F07,L35P117G07
E1685	2911057 (AL021961) caffeoyl-CoA O-methyltransferase - ... +2	797.422	1964.63	2.464	L22P24H04,L35P117G11
E3645	4586248 (AL049640) growth factor like protein [Arabido... +1 30	1718.745	4230.9	2.462	L16P7H07,L35P106B12
E1282	3063465 (AC003981) F22O13.27 [Arabidopsis thaliana] +1	961.125	2365.71	2.461	L18P27E07,L35P113D08
E1453	1353352 (U31975) alanine aminotransferase [Chlamydomon... +	3823.28	9397.64	2.458	L18P6F11,L35P115A07
E713	3063439 (AC003981) F22O13.1 [Arabidopsis thaliana] +1	618.504	1517.71	2.454	L18P11E05,L35P87F04
E3843	3893822 (U96498) ATPase beta subunit [Nicotiana sylves... +1	1605.943	3940.2	2.454	L17P21B09,L35P109A01
E3427	2961343 (AL022140) symbiosis-related like protein [Ara... +1 31	1581.058	3877.44	2.452	L16P10A01,L35P103E03
E1884	2213592 (AC000348) T7N9.12 [Arabidopsis thaliana] +3 3	2355.248	5772.73	2.451	L33P4C06,L35P119H12
E1654	1762933 (U66263) tumor-related protein [Nicotiana taba... +3 1	1216.76	2982.19	2.451	L22P13H05,L35P117B10
E1926	2462834 (AF000657) hypothetical protein [Arabidopsis t... +1 17	880.006	2153.28	2.447	L18P6H02,L35P90G06
E4379	G532	1609.162	3937.24	2.447	J121D08F1
E4050	pathogen-inducible protein CXc750	843.089	2062.27	2.446	L18P6F02F1
E1305		749.827	1833.61	2.445	L18P30A10,L35P113H07
E1261	4090884 (AF025333) vesicle-associated membrane protein... +3	1378.586	3370.44	2.445	L18P30A02,L35P113H05
E1949	4539301 (AL049480) putative mitochondrial protein [Ara... +2 21	2380.655	5816.02	2.443	L18P4E04,L35P90C11

E1179	1709794	26S PROTEASOME REGULATORY SUBUNIT S5A (M	776.228	1895.97	2.443	L17P8B05,L35P112C07
E472			313.348	765.08	2.442	L17P29H09,L35P84F08
E2764	2244973	(Z97340) similarity to extensin class 1 protei... +2	3567.583	8703.92	2.44	L24P1A12,L35P97G01
E5078	G284		778.975	1895.26	2.433	J129B03F1
E3733	3128175	(AC004521) unknown protein [Arabidopsis thaliana] +3	720.256	1751.75	2.432	L17P16A01,L35P107C10
E720			500.034	1213.58	2.427	L18P15F09,L35P87G05
E1872	4200165	(Y16262) neutral invertase [Daucus carota] +1	1044.219	2532.98	2.426	L28P2B01,L35P119F12
E169	114335	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >f	1384.304	3356.34	2.425	L17P13F06,L35P81C10
E2368			490.96	1188.29	2.42	L22P2A03,L35P95C03
E820	4204313	(AC003027) lclprt_seq No definition line four... +2	1511.947	3658.35	2.42	L18P29D04,L35P88H04
E1278			1949.806	4714.62	2.418	L18P26F02,L35P113C10
E4705	G764		235.698	569.01	2.414	J125C04F1
E3610			6321.958	15256.64	2.413	L16P9B01,L35P106E01
E1882	3540181	(AC004122) Unknown protein [Arabidopsis thaliana] +2	912.983	2201.59	2.411	L33P3H05,L35P119H10
E3469			2561.039	6173.41	2.411	L15P9G06,L35P103D09
E2451			1612.518	3883.67	2.408	L15P3E05,L35P77B01
E4747	G666		442.259	1065.12	2.408	J125A05F1
E1280	1171866	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUB	1883.53	4535.94	2.408	L18P26F12,L35P113C12
E4736	G839		1446.367	3482.65	2.408	J125G11F1
E2915	4262228	(AC006200) putative receptor protein kinase [A... +3	682.059	1642.09	2.408	L16P6A04,L35P79H11
E856			2623.425	6310.82	2.406	L18P27G05,L35P88F10
E6526	2529665	(AC002535) putative ribosomal protein L7A [Ara... +2	241.925	581.47	2.404	J44G10F1
E1875	3024697	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1	1857.054	4461.67	2.403	L28P3D06,L35P119G09
E1265	1703220	AIG2 PROTEIN >gj1127806 (U40857) AIG2 [Arabid...	2445.142	5866.67	2.399	L18P1G08,L35P113A09
E901	2369714	(Z97178) elongation factor 2 [Beta vulgaris] +1	8986.141	21538.31	2.397	L18P32B08,L35P89F01
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR		774.849	1855.44	2.395	L20P2D01F1
E3553	4544458	(AC006592) unknown protein [Arabidopsis thaliana] -1	787.08	1884.67	2.395	L16P5D07,L35P105E01
E3572	2507421	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG	2725.053	6522.72	2.394	L16P5E11,L35P105E08
E564			598.778	1432.35	2.392	L17P37A06,L35P85E11
E4380	G526		557.672	1333.98	2.392	J121E05F1
E1605	G270		711.195	1700.48	2.391	L22P12E03,L35P117B03
E88			2481.151	5930.27	2.39	L16P8H07,L35P80F07
E1555	2914703	(AC003974) unknown protein [Arabidopsis thaliana] +3	1338.972	3199.56	2.39	L20P2A07,L35P116B07
E3849	2495365	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >prf1190843	1887.569	4508.89	2.389	L17P21F10,L35P109B02
E2856			935.655	2233.82	2.387	L16P5B12,L35P79F06
E1661	1362051	protein kinase 3 - soybean >gj1310582 (L19361)... +1	633.42	1510.66	2.385	L22P18F06,L35P117C11
E3820	2661422	(AJ001342) Putative S-phase-specific ribosomal... +1	3670.192	8747.75	2.383	L17P19G11,L35P108D12

E1235		2861.124	6814.86	2.382	L18P27D06,L35P113D03
E1445		3768.178	8970.52	2.381	L20P15H02,L35P115G05
E1238	2760334 (AC002130) F1N21.5 [Arabidopsis thaliana]	4222.258	10049.8	2.38	L18P27E04,L35P113D06
E3825		425.156	1011.93	2.38	L17P1C05,L35P108E11
E4511	G859	655.695	1560.39	2.38	J123C03F1
E3320	4678226 (AC007135) putative 40S ribosomal protein S14 ... +3	1762.772	4194.1	2.379	L15P5F06,L35P102C01
E6988	4512625 (AC004793) ESTs gb T20423, gb AA712864, gb H76...	419.077	996.78	2.379	J54A12F1
E2042		645.403	1532.97	2.375	L20P11G01,L35P91C08
E3562	3914740 60S RIBOSOMAL PROTEIN L26 >dbj BAA18941 (D78	3452.705	8197.57	2.374	L16P6C05,L35P105H03
E2879		823.363	1954.39	2.374	L16P1H09,L35P79B11
E2143		1363.496	3234.23	2.372	L20P2B03,L35P92D07
E2853	730583 60S ACIDIC RIBOSOMAL PROTEIN P2 >emb CAA550	522.88	1239.76	2.371	L16P5B06,L35P79F03
E5019	G1746	684.744	1623.5	2.371	J128C05F1
E2547	3047119 (AF058919) No definition line found [Arabidops... +2 7	1594.843	3776.45	2.368	L22P8C12,L35P96B01
E1937	2506788 GERANYLGERANYL TRANSFERASE TYPE II BETA S	3346.006	7921.7	2.368	L18P34H06,L35P90A11
E2761	4093155 (AF088281) phytochrome-associated protein 1 [A... +1	944.841	2236.08	2.367	L24P10H05,L35P97F04
E1521	2244909 (Z97339) pyruvate,orthophosphate dikinase [Ara... +1	1897.675	4481.56	2.362	L20P5D12,L35P116D03
E1655		1200.104	2832.85	2.361	L22P14C07,L35P117B11
E763		858.316	2023.86	2.358	L18P15H01,L35P87G07
E2341	2618701 (AC002510) hypothetical protein [Arabidopsis t... +2 4;	1144.044	2694.13	2.355	L22P1F01,L35P94E09
E4679	G632	434.714	1020.65	2.348	J124H07F1
E4839	4544394 (AC007047) hypothetical protein [Arabidopsis t... +3 6;	964.742	2264.46	2.347	J126D07F1
E3159	4262232 (AC006200) putative ribosomal protein L7 [Arab... +2 ;	2259.313	5300.94	2.346	L15P3G08,L35P101C03
E1992		2374.241	5569.31	2.346	L20P10C03,L35P91B06
E3239		2018.283	4729.6	2.343	L15P5A10,L35P101H11
E4458	G179	106.003	248.34	2.343	J122D12F1
E5108	G760	736.055	1722.49	2.34	J129F02F1
E3012	927577 (U12927) alpha-galactosidase [Phaseolus vulgaris] +3	3468.416	8104.18	2.337	L33P3C07,L35P98H12
E3464	1168319 ACTIN 1 >gil169909 (J01298) actin [Glycine max] +2	6255.594	14606.09	2.335	L15P9D01,L35P103C10
E2280		1771.759	4132.58	2.332	L22P16F01,L35P94B06
E279	2460318 (AF021819) RNA-binding protein regulatory subu... +1	3038.91	7087.01	2.332	L17P1D04,L35P82F07
E3234	1076580 alcohol dehydrogenase homolog ADH3b - tomato >... +	478.878	1116.73	2.332	L15P4H07,L35P101G12
E4966	G1523	156.419	364.6	2.331	J127G08F1
E3372	3608142 (AC005314) putative hin1 [Arabidopsis thaliana] +2 5	5696.717	13277.42	2.331	L15P5H06,L35P102C11
E4852	G1278	536.155	1249.5	2.33	J126F09F1
E3215	3080427 (AL022604) putative protein [Arabidopsis thali... +3 56;	2247.89	5228.07	2.326	L15P4C03,L35P101D11
E2627		1208.37	2808.93	2.325	L23P1G09,L35P96H08

E5441	133872	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PREI	477.946	1079.68	2.259	J18G10F1
E1488	4371281	(AC006260) hypothetical protein [Arabidopsis t... +1 1	725.899	1639.44	2.258	L20P15B04,L35P115F12
E3185	3193285	(AF069298) T14P8.18 gene product [Arabidopsis ... +1	3504.252	7913.63	2.258	L15P4G06,L35P101G05
E946	2129944	RNA-binding protein RZ-1 - wood tobacco >dbj B... +1	4098.828	9254.98	2.258	L18P32B02,L35P89E10
E1691	4455287	(AL035527) putative protein [Arabidopsis thali... +1 23	2027.805	4574.28	2.256	L22P2D11,L35P117H11
E3831	3643604	(AC005395) receptor-like protein kinase [Arabi... -2 20	2797.917	6309.99	2.255	L17P1G05,L35P108F11
E1266			928.446	2093.44	2.255	L18P1H04,L35P113A10
E1612	1709498	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >pir	1153.591	2598.37	2.252	L22P16H05,L35P117C04
E1169	1707017	(U78721) RNA helicase isolog [Arabidopsis tha... +2 f	1423.98	3202.82	2.249	L18P17A06,L35P112H03
E2351			1308.133	2939.28	2.247	L22P21F03,L35P94G07
E2369			1090.309	2443.58	2.241	L22P2A06,L35P95C04
E2865	3184292	(AC004136) putative nucleic acid binding prote... +1 2	1247.188	2794.69	2.241	L16P5F12,L35P79H03
E2070			1550.17	3471.67	2.24	L20P15F08,L35P91G12
E5048			351.508	786.79	2.238	J128F11F1
E4660	G464		250.054	559.3	2.237	J124F09F1
E3211			2154.839	4819.73	2.237	L15P4B05,L35P101D07
E2273			1073.417	2399.72	2.236	L22P14D05,L35P94A05
E1189			1151.067	2573.31	2.236	L17P9E04,L35P112D11
E5417			485.342	1084.55	2.235	J18A10F1
E677	4512673	(AC006931) putative phosphoprotein phosphatase... +1	670.909	1498.8	2.234	L17P7F09,L35P86H10
E3621	585777	GTP-BINDING NUCLEAR PROTEIN RAN1 >gil453561	5504.835	12294.42	2.233	L17P11C02,L35P106F06
E5325	3859607	(AF104919) contains similarity to cysteine pro... +3 32	823.176	1838.08	2.233	J56E11F1
E1878	2342734	(AC002341) DNA-binding protein isolog [Arabido... +3	953.443	2127.86	2.232	L28P3G04,L35P119G12
E5043			390.836	871.85	2.231	J128F05F1
E198	2501102	SYNTAXIN-RELATED PROTEIN KNOLLE >gil118416	1919.527	4281.47	2.23	L17P17A12,L35P81H09
E3749	4337178	(AC006416) T31J12.5 [Arabidopsis thaliana] +3 4	1439.12	3203.42	2.226	L17P17F12,L35P107H09
E5111			171.845	382.48	2.226	J129F11F1
E4308	G306		209.918	466.76	2.224	J121B01F1
E2052	G1111		1055.779	2344.96	2.221	L20P13A06,L35P91D12
E392	643469	(U19886) unknown [Lycopersicon esculentum] +1	1979.601	4396.32	2.221	L17P25H04,L35P83H12
E4828	G1379		834.202	1851.49	2.219	J126C09F1
E5781			2964.952	6577.41	2.218	J28F11F1
E3231	1173218	40S RIBOSOMAL PROTEIN S15A >gil440824 (L27461	1744.214	3869.13	2.218	L15P4H03,L35P101G09
E1236	2244827	(Z97336) hypothetical protein [Arabidopsis tha... +2 41	3339.604	7406.49	2.218	L18P27D11,L35P113D04
E4939	G1232		200.508	444.62	2.217	J127A05F1
E669	1304227	(D63781) Epoxide hydrolase [Glycine max] >emb ... +1	1038.029	2301.67	2.217	L17P7B04,L35P86G08
E3830	1550738	(Y08061) endomembrane-associated protein [Arab... +	3476.881	7706.32	2.216	L17P1G04,L35P108F10

E1774	3122572	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUB	1906.413	4217.14	2.212	L23P1C04,L35P118F10
E4357	G921		491.209	1086.46	2.212	J121H09F1
E1611	2623297	(AC002409) unknown protein [Arabidopsis thalia... +1	3975.548	8789.49	2.211	L22P16B02,L35P117C03
E1347	2262098	(AC002343) HSP90 isolog [Arabidopsis thaliana] +3	1163.97	2571.05	2.209	L18P4H08,L35P114G02
E3864	4160402	(AJ132240) eukaryotic translation initiation f... +1 236	555.695	1226.32	2.207	L17P23F02,L35P109D05
E1762			665.552	1468.51	2.206	L22P9D12,L35P118D10
E3908	1172977	60S RIBOSOMAL PROTEIN L18 >gj 606970 (U15741)	318.258	701.88	2.205	L17P23H08,L35P109D07
E2425			1201.148	2648.19	2.205	L22P4D01,L35P95E11
E3291	728880	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARI	1110.309	2447.82	2.205	L34P2D10,L35P120C09
E1275	3269293	(AL030978) putative protein [Arabidopsis thali... +1 51	1736.396	3822.79	2.202	L18P26A04,L35P113C07
E3463	3123188	CATALASE 3 >gj 2347178 (U43147) catalase 3 [Ar... +:	13022.707	28658.02	2.201	L15P9C05,L35P103C09
E3190	4689473	(AC007213) putative receptor protein kinase [A... +2 4	1704.103	3748.35	2.2	L15P5A01,L35P101H04
E1185	2674203	(AF036328) CLP protease regulatory subunit CLP... +1	1239.37	2726	2.2	L17P9B11,L35P112D07
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR		482.943	1060.41	2.196	L20P2D01F1
E3271			1099.669	2413.11	2.194	L34P8G01,L35P120F01
E3860	3785983	(AC005560) hypothetical protein [Arabidopsis t... +3 9	1068.669	2343.58	2.193	L17P23C11,L35P109D01
E4925	G394		169.868	372.44	2.193	J127G02F1
E2782			1330.643	2917.1	2.192	L23P2G07,L35P97B07
E4040	cyclophilin		1409.102	3088.32	2.192	L17P3D11F1
E2766			1679.404	3680.5	2.192	L24P1C03,L35P97G03
E2757			677.087	1483.14	2.19	L23P9F05,L35P97E06
E1565	2347191	(AC002338) DNA binding protein isolog [Arabido... +3	1685.582	3690.55	2.189	L20P4B05,L35P116C11
E1866	4538920	(AL049483) nitrogen fixation like protein [Ara... +2 164	2317.834	5074.73	2.189	L28P1B07,L35P119E12
E3157			1142.056	2499.1	2.188	L15P3G05,L35P101C01
E3916	4582460	(AC007071) unknown protein [Arabidopsis thaliana] +3	905.488	1979.88	2.187	L17P25C02,L35P109E09
E4894	G743		2418.927	5284.23	2.185	J127C10F1
E3210	1546688	(X98802) peroxidase ATP11a [Arabidopsis thalia... +2	962.38	2101.1	2.183	L15P4A02,L35P101C12
E2909			948.732	2071.1	2.183	L16P5F04,L35P79G11
E5968	285286	flavonol 4'-sulfotransferase - Flaveria chlora... +2 218	844.519	1842.22	2.181	J34C08F1
E566	2213626	(AC000103) F21J9.18 [Arabidopsis thaliana] +2 1	1651.946	3602.18	2.181	L17P37G07,L35P85F07
E3415	4056502	(AC005896) 40S ribosomal protein S5 [Arabidops... +1	6229.491	13582.5	2.18	L15P9A10,L35P103C03
E6508	2088653	(AF002109) Hs1pro-1 related protein isolog [Ar... +3 5	784.532	1710.21	2.18	J44B12F1
E3868	4454026	(AL035394) phosphatase like protein [Arabidops... +1	2000.285	4357.83	2.179	L17P25B04,L35P109E03
E1468	4510375	(AC007017) putative homeotic protein BEL1 [Ara... -1	1407.647	3066.69	2.179	L20P10H03,L35P115C10
E3229	1524370	(X92491) TOM20 [Solanum tuberosum] +2 2	651.419	1418.34	2.177	L15P4H01,L35P101G07
E4505	G773		244.026	530.99	2.176	J123B04F1
E1643			634.452	1379.26	2.174	L22P26F02,L35P117H05

E4057	glutamate--ammonia ligase	1238.798	2692.59	2.174	L20P2E04F1
E4765	G620	191.981	417.26	2.173	J125E07F1
E2202		597.087	1297.71	2.173	L22P10A07,L35P93E06
E1114	G1745	400.097	869.48	2.173	L17P41D01,L35P111C10
E1432	4185513 (AF102823) actin depolymerizing factor 5 [Arab... +3 5	2172.577	4718.16	2.172	L20P13G06,L35P115E04
E2408	736704 (D49738) cytoskeleton associated protein [Homo... +1	831.331	1805.02	2.171	L22P28B04,L35P95B12
E3368	464621 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >pir S28..	3471.3	7534.93	2.171	L15P5G08,L35P102C07
E4510		264.51	573.14	2.167	J123C10F1
E3090	3785989 (AC005560) unknown protein [Arabidopsis thaliana] +3	4215.422	9129.57	2.166	L34P2F05,L35P99G06
E538		1950.316	4223.72	2.166	L17P30F08,L35P85A09
E2491		878.428	1902.34	2.166	L15P7D11,L35P77H05
E4053	endochitinase	593.607	1284.97	2.165	L18P8B07F1
E143	4105698 (AF049870) small hydrophobic protein [Arabidop... +2	1037.532	2245.16	2.164	L17P16C06,L35P81G02
E302	2529229 (AB007907) 6-phosphogluconate dehydrogenase [G... +	2234.366	4834.45	2.164	L17P20F09,L35P83A06
E3471	320556 chitinase (EC 3.2.1.14) precursor, basic - Ara... +2 630	650.051	1406.49	2.164	L15P9H03,L35P103D11
E3111	4567281 (AC006841) unknown protein [Arabidopsis thaliana] +3	2040.085	4410.94	2.162	L33P7F04,L35P99C09
E1283	3252815 (AC004705) vacuolar sorting receptor-like prot... +3 51	2060.533	4454.99	2.162	L18P27E10,L35P113D09
E1855	3695383 (AF096370) similar to inorganic pyrophosphatas... +3	1468.654	3172.51	2.16	L24P6H06,L35P119D07
E3581	2511576 (Y13177) multicatalytic endopeptidase [Arabido... +1 7	1293.378	2793.79	2.16	L16P6E09,L35P105H07
E2406		1105.039	2385.67	2.159	L22P28A08,L35P95B10
E3329	730645 40S RIBOSOMAL PROTEIN S15 >pir S43412 ribosom.	4065.417	8774.82	2.158	L15P6B09,L35P102D04
E1593		1436.286	3099.84	2.158	L22P10A10,L35P116H09
E3295		2080.433	4490.01	2.158	L34P4F04,L35P120D07
E1145		2155.113	4650.82	2.158	L17P9A01,L35P112D03
E3667	2529665 (AC002535) putative ribosomal protein L7A [Ara... +2	4890.631	10545.88	2.156	L17P11H05,L35P106F10
E4502	G804	505.888	1090.58	2.156	J123B10F1
E4710	G1241	733.059	1579.88	2.155	J125D10F1
E2606		1584.824	3414.99	2.155	L22P9D09,L35P96D07
E2748		1223.509	2634.2	2.153	L23P6B07,L35P97D03
E969	2702268 (AC003033) putative cellulase [Arabidopsis tha... +3 3	1025.711	2207.56	2.152	L17P28B01,L35P110A03
E4498	G702	200.11	430.62	2.152	J123A12F1
E2398	2104683 (X97908) transcription factor [Vicia faba] +1 357	802.443	1726.39	2.151	L22P6F10,L35P95H03
E5147		588.784	1266.61	2.151	J129E07F1
E3041		1004.157	2159.77	2.151	L34P8G07,L35P100B11
E2538	2129899 chalcone reductase homolog - Sesbania rostrata... +1	1819.764	3912.52	2.15	L15P7G02,L35P77H10
E1796		925.351	1988.97	2.149	L24P10B02,L35P119B02
E2391	2252854 (AF013294) similar to auxin-induced protein [A... +1 1	1627.584	3496.94	2.149	L22P6C05,L35P95G02

E6020	1723239	HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHF	419.587	901.27	2.148	J34H12F1
E3483	4455235	(AL035523) PROTEIN TRANSPORT PROTEIN SEC61	4100.494	8804.03	2.147	L16P10G01,L35P103F11
E5076	G28		1573.961	3378.84	2.147	J129B02F1
E2429	4512664	(AC006931) putative ribose phosphate pyrophosp... +2	397.201	852.09	2.145	L22P5H09,L35P95F09
E521			1257.108	2695.84	2.144	L17P37D02,L35P85F03
E4960	G1713		227.084	486.93	2.144	J127F06F1
E1985			945.276	2026.53	2.144	L18P8F06,L35P91A05
E1500	2088653	(AF002109) Hs1pro-1 related protein isolog [Ar... +3 5	2620.554	5617.62	2.144	L20P1A07,L35P115H12
E1724			300.831	643.74	2.14	L23P12F07,L35P118F02
E1101	127045	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIC	1501.332	3212.64	2.14	L17P3A07,L35P111A08
E1579	118619	SUCCINATE DEHYDROGENASE (UBIQUINONE) IROI	1317.182	2817.86	2.139	L21P1F04,L35P116F07
E4683	G660		1438.486	3074.89	2.138	J125A01F1
E2743	3152621	(AC004482) cold acclimation protein WCOR413-li... +2	1768.44	3780.12	2.138	L23P3D08,L35P97C04
E1832			5688.065	12148.83	2.136	L28P4E07,L35P119H02
E4856	G378		435.945	931.03	2.136	J126F11F1
E1543	1170028	GLUTAMATE-1-SEMIALDEHYDE 2, 1-AMINOMUTASE	2243.192	4790.25	2.135	L21P8B05,L35P116H01
E1303			2560.082	5457.98	2.132	L18P2G12,L35P113G11
E1650			492.874	1050.73	2.132	L22P12C01,L35P117A12
E1562	3164138	(D78604) cytochrome p450 monooxygenase [Arabid...	1158.215	2469.11	2.132	L20P2G05,L35P116C08
E3124			2277.822	4855.72	2.132	L34P1E08,L35P99E10
E2297	1778095	(U64903) putative sugar transporter; member of... +3 ;	4428.944	9439.68	2.131	L22P1E02,L35P94E05
E1449	1046225	(U21952) ethylene response sensor [Arabidopsis... +3	1768.888	3769.85	2.131	L20P17B08,L35P115H03
E1935	4210330	(AJ223802) 2-oxoglutarate dehydrogenase, E1 su... +2	3572.654	7611.53	2.13	L18P34G06,L35P90A09
E5422	1168748	CALMODULIN-4 >pir S35185 calmodulin 4 - Arabi... +2	1110.048	2363.31	2.129	J18B11F1
E551			1805.457	3843.1	2.129	L17P32G10,L35P85C10
E2682	3702964	(AF079485) rac GTP binding protein Arac10 [Ara... +1	2377.647	5057.39	2.127	L15P8B04,L35P78A09
E5015			309.32	657.58	2.126	J128B07F1
E548			2167.083	4602.66	2.124	L17P32E09,L35P85C07
E2377			822.182	1746.03	2.124	L22P2G04,L35P95D06
E2512			1607.708	3413.64	2.123	L15P4H09,L35P77D08
E1486			1765.209	3747.91	2.123	L20P14H07,L35P115F10
E3144	4454472	(AC006234) unknown protein [Arabidopsis thaliana] +1	2387.529	5068.22	2.123	L34P4G03,L35P99H12
E6947	730645	40S RIBOSOMAL PROTEIN S15 >pir S43412 ribosom.	776.291	1647.64	2.122	J51H04F1
E3261	2894599	(AL021889) putative protein [Arabidopsis thali... +1 58	4151.73	8809.88	2.122	L34P3G03,L35P120D03
E1209	1495269	(X97829) product similar to ccr protein, Citru... +1 387	2150.476	4555.47	2.118	L18P17E02,L35P112H07
E3462	G860		1541.755	3265.62	2.118	L15P9C02,L35P103C08
E1464	G512		984.729	2085.73	2.118	L18P9B08,L35P115B12

E4774	G301	334.243	707.32	2.116	J125G08F1
E4766	G563	419.463	887.65	2.116	J125E08F1
E759		2697.595	5708.38	2.116	L18P15C02,L35P87F09
E521		657.771	1391.33	2.115	L17P37D02,L35P85F03
E3739	3450889 (AF083890) 19S proteasome subunit 9 [Arabidops... +3	1482.165	3134.05	2.115	L17P17A03,L35P107F09
E4336	G519	1541.27	3253.09	2.111	J121E03F1
E2210	2943789 (AB000875) RD22BP1 [Arabidopsis thaliana] +1 ;	1947.855	4110.53	2.11	L22P11G06,L35P93G02
E2781	1170203 GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GL	1513.352	3192.79	2.11	L23P2D09,L35P97A12
E1269	3335333 (AC004512) Similar to chloroplast membrane-ass... +2	2124.783	4472.16	2.105	L18P23D02,L35P113B07
E4017	UBIQUITIN-CONJUGATING ENZYME	466.796	982.07	2.104	L15P9G10F1
E1834	4406780 (AC006532) putative multispinning membrane pro... +2	1854.158	3899.35	2.103	L33P3B02,L35P119H04
E1409	133709 CYANELLE 30S RIBOSOMAL PROTEIN S10 >pir R3K	2422.817	5089.72	2.101	L18P6E05,L35P115A05
E4025	CELL DIVISION CYCLE PROTEIN 48	927.738	1945.98	2.098	L16P11D01F1
E1644		1399.22	2934.35	2.097	L22P28B06,L35P117H06
E3508	4193382 (AF083336) ribosomal protein S27 [Arabidopsis ... +3	2651.231	5558.39	2.097	L16P1G05,L35P104D06
E1489		1333.092	2794.08	2.096	L20P16B07,L35P115G07
E5101		302.459	633.89	2.096	J129E10F1
E4069	caffeic o-methyltransferase	805.165	1687.13	2.095	L34P4G06F1
E1873	G1398 (similar to remorin 1)	1100.838	2304.93	2.094	L28P2H04,L35P119G07
E3721	2829891 (AC002311) Unknown protein [Arabidopsis thaliana] +2	409.842	858.09	2.094	L17P14D11,L35P107A10
E6744		497.883	1041.47	2.092	J46C06F1
E2292		2303.117	4817.58	2.092	L22P1A07,L35P94D06
E757		1150.334	2405.79	2.091	L18P15A05,L35P87F07
E4526	G1125	1400.686	2928.99	2.091	J123E10F1
E3725	3892714 (AL033545) trehalose-6-phosphate phosphatase -... +1	2128.786	4450.72	2.091	L17P15C09,L35P107B08
E2896	2739383 (AC002505) unknown protein [Arabidopsis thaliana] +1	1579.306	3299.84	2.089	L16P5A03,L35P79E10
E1229		240.148	501.65	2.089	L18P25C09,L35P113C03
E3550		5788.835	12070.32	2.085	L16P5B01,L35P105C04
E3208	4586109 (AL049638) putative protein [Arabidopsis thali... +3 27.	5072.706	10576.02	2.085	L15P3H08,L35P101C10
E2436	2578442 (X67426) pectinesterase [Pisum sativum] +2 11	1518.162	3164.27	2.084	L22P6E11,L35P95G10
E1447	2832241 (AF030864) nonphototropic hypocotyl 1 [Arabido... +2	4618.825	9624.53	2.084	L20P16H05,L35P115H01
E1471		2029.234	4227.41	2.083	L20P11G04,L35P115D07
E985	1174870 UBIQUINOL-CYTOCHROME C REDUCTASE COMPL	1615.949	3365.97	2.083	L17P2H04,L35P110D01
E855	3608412 (AF079355) protein phosphatase-2c [Mesembryant... +;	2227.555	4639.52	2.083	L18P27G03,L35P88F09
E2752	1362162 beta-glucosidase BGQ60 precursor - barley >gil... +3 ;	4572.784	9520.91	2.082	L23P9B01,L35P97E01
E1735	2351374 (U54560) putative 26S proteasome subunit athMO... +1	1149.514	2392.79	2.082	L23P2G02,L35P118H01
E3738	4127456 (AJ010818) Cpn21 protein [Arabidopsis thaliana] +2 ;	4289.48	8927.44	2.081	L17P16F09,L35P107E09

E6201	2511598 (Y13696) multicatalytic endopeptidase complex,... +2 ;	680.02	1414.87	2.081	J37F05F1
E4712	G1023	221.217	460.13	2.08	J125D11F1
E338	3915847 40S RIBOSOMAL PROTEIN S2 >gij2335095 (AC00233)	632.538	1314.6	2.078	L17P25A05,L35P83G06
E5135		1072.51	2228.46	2.078	J129B07F1
E1647		911.579	1893.87	2.078	L22P11G05,L35P117A09
E2343	541849 anthranilate synthase (EC 4.1.3.27) beta chain... +3 36	2272.017	4720.09	2.077	L22P1F05,L35P94E11
E4854	G1366	591.307	1228.15	2.077	J126F10F1
E4503	G859	583.899	1212.3	2.076	J123B03F1
E4680	G656	375.485	779.37	2.076	J124H11F1
E1073		947.104	1964.64	2.074	L17P40B02,L35P111C02
E4492	G1390	322.608	668.69	2.073	J123A09F1
E2618		1265.088	2620.9	2.072	L23P12E08,L35P96F08
E4007	CYSTEINE PROTEINASE 2 PRECURSOR	458.17	949.15	2.072	L15P6D02F1
E191	2459438 (AC002332) hypothetical protein [Arabidopsis thaliana] +1 2	1640.623	3395.79	2.07	L17P16E03,L35P81G08
E1778		730.635	1511.54	2.069	L23P2D03,L35P118G08
E3008	2341039 (AC000104) Similar to Nicotiana lesion-inducin... +1 4	4083.452	8446.91	2.069	L33P3B01,L35P98H08
E1391	2739389 (AC002505) Cf-2.2 like protein [Arabidopsis thaliana] +1 57	2451.344	5065.38	2.066	L18P4G06,L35P114F11
E690		1187.288	2453.06	2.066	L17P9B10,L35P87B05
E4050	pathogen-inducible protein CXc750	2748.309	5677.92	2.066	L18P6F02F1
E4468	G1352	433.956	896.08	2.065	J122F09F1
E2403	2642432 (AC002391) putative elicitor response element ... +2 2	1748.751	3610.71	2.065	L22P26E08,L35P95B07
E1798	4335735 (AC006248) hypothetical protein [Arabidopsis thaliana] +2 3	796.576	1643.14	2.063	L24P12A01,L35P119B04
E3082	4567260 (AC006841) putative NADPH dependent mannose 6-phosphate isomerase +2 404	2439.411	5030.77	2.062	L34P1G10,L35P99F04
E1792	3717946 (AJ005901) vag1 [Arabidopsis thaliana]	3429.697	7070.1	2.061	L23P7B01,L35P119A04
E2456		3200.078	6595.41	2.061	L15P3G11,L35P77B06
E4071	cruciferin 1	632.239	1302.29	2.06	L34P9H04F1
E2014	3128195 (AC004521) putative phosphoribosyl pyrophosphatase... +1	1524.626	3138.81	2.059	L20P14D03,L35P91F04
E1149	4006829 (AC005970) putative protein kinase [Arabidopsis thaliana] +3 4	977.557	2011.9	2.058	L17P9G03,L35P112E01
E2054		3046.865	6270.71	2.058	L20P14A07,L35P91E08
E4556	G658	303.329	624.13	2.058	J123A06F1
E2065	3810848 (AL032684) putative autophagy protein [Schizosaccharomyces pombe] +1 ;	2845.624	5851.22	2.056	L20P15C08,L35P91G07
E2727	4678226 (AC007135) putative 40S ribosomal protein S14 ... +2	1158.463	2381.64	2.056	L16P1B03,L35P78H12
E2212		1417.479	2913.56	2.055	L22P12C03,L35P93G04
E2214	4455293 (AL035528) putative protein [Arabidopsis thaliana] +1 27	1134.399	2331.57	2.055	L22P12E05,L35P93G06
E3384	1351359 UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX +1	1798.558	3696.64	2.055	L15P7C04,L35P102E11
E3319	3024434 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG +1	986.072	2026.31	2.055	L15P5E02,L35P102B06
E3895	4467128 (AL035538) putative protein [Arabidopsis thaliana] +3 47	716.875	1472.32	2.054	L17P21F01,L35P109A12

E1861	3287693 (AC003979) Similar to LIM17 gene product gb 16... +2	2338.666	4801.31	2.053	L24P9E08,L35P119E07
E2601	135535 T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-AL	2325.776	4774.42	2.053	L22P8H07,L35P96C08
E4519	G1009	215.946	442.81	2.051	J123D03F1
E1187	1841355 (D85381) cytochrome c oxidase subunit Vb precu... +1	940.13	1927.06	2.05	L17P9D02,L35P112D09
E1157	2809245 (AC002560) F21B7.14 [Arabidopsis thaliana] +2 8	1393.117	2855.11	2.049	L18P10E06,L35P112F03
E2098	3702336 (AC005397) putative 3-methyl-2-oxobutanate hy... +1	871.33	1785.16	2.049	L20P1H05,L35P92D04
E2450	4646206 (AC007230) Contains similarity to gb D13630 Kl... +3 ;	1856.084	3802.35	2.049	L15P3B02,L35P77A06
E2829	4567201 (AC007168) putative aspartate aminotransferase... +1	5126.379	10497.97	2.048	L16P1G01,L35P79B03
E5411	4455223 (AL035440) putative DNA binding protein [Arabi... +3 ;	785.352	1607.49	2.047	J18G08F1
E3919	3128228 (AC004077) putative ribosomal protein L18A [Ar... +1 ;	1340.563	2742.47	2.046	L17P25C10,L35P109E12
E669	1304227 (D63781) Epoxide hydrolase [Glycine max] >emb ... +1	1660.871	3396.49	2.045	L17P7B04,L35P86G08
E4109	GP-39	5938.53	12138.75	2.044	O17203,M80927
E3378	421941 GTP-binding protein, ras-related - common toba... +3 ;	4026.051	8229.36	2.044	L15P6D11,L35P102D11
E3110		1075.07	2196.51	2.043	L33P7E03,L35P99C08
E3293		437.014	892.06	2.041	L34P2E04,L35P120C11
E2431		2207.157	4502.44	2.04	L22P6A09,L35P95F11
E1126		1157.941	2361.03	2.039	L17P5H03,L35P111E10
E1824		1093.131	2226.94	2.037	L28P1F03,L35P119F06
E2200		654.191	1331.93	2.036	L22P10A04,L35P93E04
E333		1206.828	2456.71	2.036	L17P23H04,L35P83G01
E1816	4103987 (AF030516) 5,10-methylenetetrahydrofolate dehy... +1	5051.749	10282.53	2.035	L24P9A06,L35P119E04
E2564		1186.928	2414.88	2.035	L22P9D08,L35P96D06
E2478	4432856 (AC006300) putative 2A6 protein [Arabidopsis t... +1 1	2534.973	5157.41	2.035	L15P5G07,L35P77F04
E1796		1494.719	3039.63	2.034	L24P10B02,L35P119B02
E2146	1170409 HOMEBOX-LEUCINE ZIPPER PROTEIN HAT22 (HC	1511.226	3071.03	2.032	L20P2C01,L35P92D10
E3151	2499811 PROFILIN 2 >gi 1353766 (U43323) profilin 2 [Ar... +1 ;	5361.032	10890.84	2.031	L15P3C10,L35P101B01
E517	4204311 (AC003027) lclprt_seq No definition line four... +2 64;	650.574	1320.81	2.03	L17P36F06,L35P85E05
E644	4753657 (AL049751) putative protein [Arabidopsis thali... +3 33	576.814	1170.05	2.028	L17P41D03,L35P86C07
E1885	1084415 RNA-binding protein - Wood tobacco >dbj BAA051... +2	3681.367	7465.9	2.028	L18P34F02,L35P90A01
E0	NUL	186.363	377.79	2.027	NUL
E533		1675.265	3394.21	2.026	L17P3B11,L35P85H04
E2976	1173351 DNA BINDING PROTEIN S1FA >pir S47063 s1Fa pro.	2964.591	5989.77	2.02	L24P9F06,L35P98B12
E4309		225.057	454.62	2.02	J121B09F1
E2207	3688173 (AL031804) putative protein [Arabidopsis thali... +2 47	928.086	1874.12	2.019	L22P11B08,L35P93F05
E1461		1155.853	2333.24	2.019	L18P9A02,L35P115B09
E2689	4678261 (AL049657) putative proteasome regulatory subu... +2	2133.509	4303.84	2.017	L15P8E08,L35P78B10
E579		597.038	1203.67	2.016	L17P3C09,L35P85H08

Dotrytis 12 hrs.

EXHIBIT E

Coord	EID	ANNOTATION cy3_cut 6378.88 cy5_cut 6073.95	N.Cy3	Cy5	N.Cy3/Cy5	Cy5/N.Cy3	lg2(N.3/5)
4_1_22_1	E0		886.84	28.22	31.42	0.03	4.97
1_1_9_17	E5137	2129662 ovule-specific homeotic protein homolog A20 - ... +3 141 8	957.03	45.26	21.15	0.05	4.4
1_1_17_6	E3171	481821 probable glutathione transferase (EC 2.5.1.18)... +3 586 3.6	37174.02	1936.59	19.2	0.05	4.26
4_4_11_5	E53		684.54	39.7	17.24	0.06	4.11
3_1_22_19	E7257		2754.52	312.13	8.82	0.11	3.14
1_2_15_8	E2343	541849 anthranilate synthase (EC 4.1.3.27) beta chain... +3 367 1.9	7420.95	913.06	8.13	0.12	3.02
3_1_21_23	E7183	G1537	2484.58	378.37	6.57	0.15	2.72
2_4_15_13	E2623	4467097 (AL035538) heat shock protein 70 like protein ... +3 584 5.1	3715.08	603.15	6.16	0.16	2.62
3_1_1_15	E4060	"chlorate/nitrate transporter,"	1431.23	234.47	6.1	0.16	2.61
2_3_19_22	E1454	3688186 (AL031804) putative protein [Arabidopsis thali... +3 676 1.1	8146.8	1338.85	6.08	0.16	2.61
4_1_7_11	E4349	G921	1620.41	270	6	0.17	2.59
2_2_20_8	E1525	2160152 (AC000375) ESTs gb U75592.gb T13956.gb T43869 ... +2	7303.89	1299.66	5.62	0.18	2.49
4_2_7_11	E4357	G921	2627.14	471.47	5.57	0.18	2.48
3_4_8_15	E4794	G915	11557.62	2143	5.39	0.19	2.43
3_3_22_4	E7204	G1420	499.89	93.83	5.33	0.19	2.41
2_3_7_21	E4564	G920	777.56	152.68	5.09	0.2	2.35
4_1_13_23	E2049	3851530 (AF065435) nodulin [Glycine max] +3 640 6.8e-1	7283.43	1541.02	4.73	0.21	2.24
1_1_10_4	E5114	G915	17693.16	3799.43	4.66	0.21	2.22
1_2_8_16	E4827	G186	7865.42	1726.66	4.56	0.22	2.19
1_3_11_19	E123	3882356 (U92460) 12-oxophytodienoate reductase OPR2 [A... +3 53	4076.81	897.31	4.54	0.22	2.18
1_2_19_20	E1312	3738340 (AC005170) GMP synthase-like protein [Arabidop... +2 472	16921.24	3731.98	4.53	0.22	2.18
1_4_16_18	E3313	464367 POLYGALACTURONASE INHIBITOR PRECURSOR (POLY	9413.85	2106.11	4.47	0.22	2.16
1_1_9_13	E5067		7702.47	1753.09	4.39	0.23	2.14
1_2_21_21	E7448		8179.46	1861.13	4.39	0.23	2.14
3_1_20_23	E1669	3834312 (AC005679) Strong similarity to glycoprotein E... +1 595 1.1	25818.04	5998.3	4.3	0.23	2.11
4_4_12_13	E784	3420008 (AF000307) steroid sulfotransferase 3 [Brassic... +1 211 2.	10178.32	2385.71	4.27	0.23	2.09
1_2_21_22	E7450		15610.84	3692.83	4.23	0.24	2.08
4_4_13_13	E2084	4587610 (AC006951) putative indole-3-glycerol phosphat... +2 413 5	9299.15	2244.55	4.14	0.24	2.05
1_2_14_2	E1909		21686.4	5464.56	3.97	0.25	1.99
2_3_12_21	E741	3914996 PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR	9856.65	2493.14	3.95	0.25	1.98
2_4_20_5	E1562	3164138 (D78604) cytochrome p450 monooxygenase [Arabid... +3 3	10802.32	2744.4	3.94	0.25	1.98
1_4_14_7	E1962		23965.51	6123.9	3.91	0.26	1.97
1_4_21_5	E1704	3928099 (AC005770) unknown protein [Arabidopsis thaliana] +2 380	10472.11	2679.08	3.91	0.26	1.97
2_3_10_20	E2884		4262.66	1094.31	3.9	0.26	1.96
1_3_7_19	E4493	G626	2226.28	576.05	3.86	0.26	1.95
3_1_7_14	E4413	G29	1936.76	511.28	3.79	0.26	1.92

4_1_5_6	E6700	2827546 (AL021635) cytochrome P450 like protein [Arabi... +2 853	18637.8	4979.11	3.74	0.27	1.9
2_4_18_9	E3822	3193296 (AF069298) similar to pectinesterase [Arabidop... +3 700 1	3429.65	922.82	3.72	0.27	1.89
3_1_20_12E1295		452470 (U05218) ATP sulfurylase [Arabidopsis thaliana] +2 727 4.	22361.9	6019.52	3.71	0.27	1.89
1_2_21_12E1843			6645.83	1795.4	3.7	0.27	1.89
1_4_15_13E2354			3257.25	881.63	3.69	0.27	1.89
2_4_7_22	E4570	G1043	909.2	250.02	3.64	0.27	1.86
2_2_14_3	E2103	3021273 (AL022347) serine/threonine kinase - like prot... +2 543 1.3	1471.6	405.15	3.63	0.28	1.86
3_1_19_11E3922		1086263 TMV resistance protein N - tobacco (Nicotiana ... +3 262 1.	3114.44	864.4	3.6	0.28	1.85
2_4_13_16E2126			2969.76	830.85	3.57	0.28	1.84
2_4_7_13	E4408	G350	2726.62	768.74	3.55	0.28	1.83
2_4_14_2	E2102	4512651 (AC007048) putative tyrosine transaminase [Ara... +2 648	8519.84	2397.45	3.55	0.28	1.83
1_4_16_7	E2990		3674.18	1037.57	3.54	0.28	1.82
3_1_21_14E1865		3367517 (AC004392) Similar to F411.26 putative beta-gl... +2 697 6.	3209.07	917.98	3.5	0.29	1.81
1_4_10_21E2697		3738287 (AC005309) glutathione s-transferase, GST6 [Ar... +2 680	6208.81	1841.93	3.37	0.3	1.75
1_4_1_1	E4001		436.47	130.05	3.36	0.3	1.75
1_1_12_16E538			14828.76	4443.63	3.34	0.3	1.74
2_2_7_19	E4515	G1004	957.42	286.35	3.34	0.3	1.74
2_4_9_18	E7385	G1468	8179.27	2461.52	3.32	0.3	1.73
3_4_19_16E1056		4559358 (AC006585) putative steroid binding protein [A... +3 203 1.	9817.91	2973.44	3.3	0.3	1.72
1_3_17_6	E3172	1170089 GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) +2	15815.37	4827.44	3.28	0.31	1.71
3_1_9_20	E5095	G515	504.42	153.57	3.28	0.3	1.72
3_2_21_21E7460			7271.88	2230.11	3.26	0.31	1.71
2_3_21_8	E1758	2129600 glutathione synthase (EC 6.3.2.3) 2 - Arabidop... +2 441 8.	6460.75	2011.94	3.21	0.31	1.68
3_4_11_20E269			10588.89	3295.03	3.21	0.31	1.68
2_2_13_15E2081		4680337 (AF128457) hypothetical protein [Oryza sativa ... +1 234 1.	7588.93	2375.2	3.2	0.31	1.68
2_3_1_19	E4069	caffeic o-methyltransferase	7206.52	2284.74	3.15	0.32	1.66
3_2_21_4	E1725		2228.88	730.72	3.05	0.33	1.61
2_3_10_10E2822		112785 DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLAD	7255.46	2390.11	3.04	0.33	1.6
2_4_16_21E2822		112785 DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLAD	9056.4	2988.64	3.03	0.33	1.6
1_2_10_15E2684			9656.22	3205.93	3.01	0.33	1.59
1_2_22_2	E7456		6189.7	2071.78	2.99	0.33	1.58
4_4_13_14E2086			11985.51	4004.9	2.99	0.33	1.58
3_4_13_17E1942		2832663 (AL021710) hypothetical protein [Arabidopsis t... +2 239 2.	15793.4	5294.33	2.98	0.34	1.58
2_4_7_16	E4457	G195	855.5	291.3	2.94	0.34	1.55
2_3_14_20E2367		3122858 D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECUF	5505.02	1890.07	2.91	0.34	1.54
2_4_12_7	E432		10416.78	3582.26	2.91	0.34	1.54
1_3_19_2	E3857	3776578 (AC005388) ESTs gb F13915 and gb F13916 come f... +2	11930.52	4122.97	2.89	0.35	1.53

1_3_15_22E2743	3152621 (AC004482) cold acclimation protein WCOR413-li... +2 491	9846.11	3762.33	2.62	0.38	1.39
2_3_15_9 E2391	2252854 (AF013294) similar to auxin-induced protein [A... +1 190 3.	8564.9	3285.36	2.61	0.38	1.38
3_3_9_9 E5076	G28	5392.72	2068.28	2.61	0.38	1.38
4_1_8_2 E4611	G555	913.84	350.29	2.61	0.38	1.38
1_1_12_12E489		6846.79	2636.96	2.6	0.39	1.38
1_2_13_21E1901		9420.8	3630.3	2.6	0.39	1.38
1_3_1_19 E4069	caffeic o-methyltransferase	10995.37	4221.25	2.6	0.38	1.38
2_4_14_14E2542	3434969 (AB008104) ethylene responsive element binding... +2 422	7289.2	2806.68	2.6	0.39	1.38
1_1_12_23E552		11417.89	4402.5	2.59	0.39	1.37
1_3_9_4 E4737	G271	3427.1	1323.33	2.59	0.39	1.37
1_1_14_5 E943		11001.57	4257.53	2.58	0.39	1.37
1_2_9_1 E4844	G1006	4117.54	1605.18	2.57	0.39	1.36
1_3_21_4 E1696	2262100 (AC002343) unknown protein [Arabidopsis thaliana] +1 429	10141.27	3942.7	2.57	0.39	1.36
1_3_10_18E2462	1208408 (D14824) nitrite reductase [Arabidopsis thalia... +3 137 1.6	3732.49	1459.32	2.56	0.39	1.35
1_4_10_12E2637	2651316 (AC002336) unknown protein [Arabidopsis thaliana] -2 113	3817.08	1492.45	2.56	0.39	1.35
3_1_10_17E2465		8455.27	3307.84	2.56	0.39	1.35
3_1_21_7 E1767		12958.61	5066.78	2.56	0.39	1.35
1_4_21_23E7453		5817.12	2279.87	2.55	0.39	1.35
1_3_11_8 E2530		5030.97	1984.43	2.54	0.39	1.34
1_1_16_5 E2754	2980766 (AL022198) putative calmodulin-binding protein... +2 491 4	8791.1	3470.21	2.53	0.39	1.34
4_1_10_11E2829	4567201 (AC007168) putative aspartate aminotransferase... +1 109	1364.43	540.17	2.53	0.4	1.34
4_4_14_17E2595	4206196 (AF071527) hypothetical protein [Arabidopsis t... +2 272 5.	7667.19	3034.14	2.53	0.4	1.34
1_3_21_13E1840	1171991 PHENYLALANINE AMMONIA-LYASE 1 >pir S52990 phe... .	16934.48	6729.96	2.52	0.4	1.33
1_4_12_11E290		15016.19	5987.17	2.51	0.4	1.33
1_2_3_23 E5917	2062169 (AC001645) ABC transporter (PDR5-like) isolog ... +1 237	41166.34	16441.5	2.5	0.4	1.32
1_3_10_14E2496	2497753 NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSO	5431.44	2169.62	2.5	0.4	1.32
3_1_10_15E2503	510876 (X80051) NADP dependent malic enzyme [Phaseolu... +1 1	6324.08	2526.8	2.5	0.4	1.32
3_2_22_1 E0		466.9	186.46	2.5	0.4	1.32
1_4_19_12E1042	2924785 (AC002334) similar to disease resistance prote... +2 250 1	1849.62	744.09	2.49	0.4	1.31
3_4_11_6 E2677		11264.39	4530.91	2.49	0.4	1.31
2_1_2_18 E5609	2129755 tryptophan synthase (EC 4.2.1.20) alpha chain ... +1 561 8	17043.36	6870.23	2.48	0.4	1.31
3_1_11_5 E2487	3915085 TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC A	8504.09	3426.41	2.48	0.4	1.31
1_2_14_22E2285	1363482 IAA11 protein - Arabidopsis thaliana >gil97292... +3 434 4.	7643.69	3097.61	2.47	0.41	1.3
2_1_17_17E3682	115486 CALMODULIN-2/3/5 >pir S22503 calmodulin - Ara... +2 592	14519	5873.99	2.47	0.4	1.31
2_4_7_17 E4454	G187	1205.55	487.74	2.47	0.4	1.31
4_2_10_16E28		7421.43	3010.28	2.47	0.41	1.3
1_3_15_23E2745		8461.8	3440.08	2.46	0.41	1.3

1_2_15_15E2967	2160190 (AC000132) No definition line found [Arabidops... +2 455 2	9954.85	4064.31	2.45	0.41	1.29
1_4_16_3 E2982	2584721 (Y10157) sulfite reductase [Arabidopsis thaliana] +1 497 2.	26468.04	10802.41	2.45	0.41	1.29
1_3_9_13 E5069	G189	10259.39	4196.51	2.44	0.41	1.29
2_3_21_7 E1756	G22	1420.49	583.36	2.44	0.41	1.28
2_4_13_13E2078	gij3033375 putative berberine bridge enzyme from Arabidopsis thalian	15568.05	6418.88	2.43	0.41	1.28
4_1_11_14E351		9217.44	3799.65	2.43	0.41	1.28
4_1_14_5 E2059	2924777 (AC002334) putative receptor protein kinase [A... +2 116 2	9719.27	4006.79	2.43	0.41	1.28
2_2_15_22E3027	3850571 (AC005278) Similar to gb U85207 snRNP core Sm ... +2 35	10033.66	4146.96	2.42	0.41	1.27
2_3_20_16E1446	3766368 (AL031907) putative trascription factor, ccr4-... +1 157 3.7e	9031.76	3736.72	2.42	0.41	1.27
3_1_19_18E3936		7720.19	3192.52	2.42	0.41	1.27
1_1_12_20E505	3367524 (AC004392) F8K4.12 [Arabidopsis thaliana] +3 284 3.	8302.41	3450.52	2.41	0.42	1.27
2_2_2_11 E5714	3164138 (D78604) cytochrome p450 monooxygenase [Arabid... +2 7	9774.11	4050.3	2.41	0.41	1.27
1_1_12_14E493	4218011 (AC006135) putative protein kinase [Arabidopsi... +2 378 1	5397.13	2249.36	2.4	0.42	1.26
1_1_16_8 E1796		8385.09	3498.53	2.4	0.42	1.26
2_1_13_10E763		5108.43	2132.61	2.4	0.42	1.26
4_4_10_11E19	G1145	7179.61	2992.49	2.4	0.42	1.26
1_1_19_23E1265	1703220 AIG2 PROTEIN >gij1127806 (U40857) AIG2 [Arabid... +2 5	9661.9	4037.36	2.39	0.42	1.26
1_2_12_16E634	4583153 (AF108211) cytosolic inorganic pyrophosphatase... +1 243	13267.86	5557.51	2.39	0.42	1.26
1_4_11_17E215	2352828 (AF009228) NaCl-inducible Ca2+-binding protein... +3 518	6871.98	2874.02	2.39	0.42	1.26
2_2_19_10E1191		7669.07	3214.05	2.39	0.42	1.25
4_2_12_20E797		5589.18	2337.69	2.39	0.42	1.26
4_2_16_4 E7102	G619	2027.69	847.01	2.39	0.42	1.26
4_4_13_15E2096	2440035 (X98544) endo-1,4-beta-glucanase [Arabidopsis ... +2 743	13570.65	5668.97	2.39	0.42	1.26
2_1_15_12E2433		8196.36	3445.65	2.38	0.42	1.25
2_4_17_13E2884		3734.31	1566.63	2.38	0.42	1.25
2_4_21_18E3296	2781394 (U70424) O-methyltransferase 1 [Arabidopsis th... +3 325	9323.53	3922.33	2.38	0.42	1.25
3_1_21_1 E1671	4006918 (Z99708) peroxidase like protein [Arabidopsis ... +2 700 3.(6719.76	2826.5	2.38	0.42	1.25
1_1_8_23 E4765	G620	234.26	98.88	2.37	0.42	1.24
2_4_14_15E2544		7301.69	3086.91	2.37	0.42	1.24
2_4_20_6 E1564	3434967 (AB008103) ethylene responsive element binding... +1 272	7292.96	3078.58	2.37	0.42	1.24
3_4_11_5 E2675	1076211 hypothetical protein VSP-3 - Chlamydomonas rei... +2 184	8982.65	3783.32	2.37	0.42	1.25
3_2_8_23 E4855	G1383	3817.16	1617.13	2.36	0.42	1.24
1_1_15_6 E2245	1706917 FLAVONOL SULFOTRANSFERASE-LIKE >pir S69188 fl...	6547.54	2787.07	2.35	0.43	1.23
1_1_19_17E3928	4263771 (AC006218) putative nonspecific lipid-transfer... +1 491 4.2	5274.81	2243.56	2.35	0.43	1.23
1_2_20_22E1607	2660677 (AC002342) unknown protein [Arabidopsis thaliana] +2 663	3920.89	1665.6	2.35	0.42	1.24
2_4_13_23E2140		7926.91	3369.18	2.35	0.43	1.23
3_3_13_17E928		10353.41	4409.1	2.35	0.43	1.23

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EXHIBIT F

EID	COMMENT	(0.944)CY3	CY5	CY5/(0.944)CY3	SOURCE
E2067	417527 PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (F	543.622	38569.4	70.949	L20P15F02,L35P91G09
E3713	4105794 (AF049928) PGP224 [Petunia x hybrida]	573.554	18153.35	31.651	L17P17D04,L35P107H01
E2050		1336.744	35150.66	26.296	L20P13A01,L35P91D10
E3171	481821 probable glutathione transferase (EC 2.5.1.18)... +3	1595.128	36546.61	22.911	L15P4C09,L35P101E03
E822	2281113 (AC002333) endochitinase isolog [Arabidopsis t...	817.426	9283.46	11.357	L18P29E04,L35P88H06
E5077	G354	437.549	4633.87	10.591	J129B10F1
E4591	G263	656.994	6703.33	10.203	J124B01F1
E2049	3851530 (AF065435) nodulin [Glycine max]	2295.556	23292.02	10.147	L20P12H08,L35P91D09
E1197		650.772	6511.07	10.005	L18P10G01,L35P112F07
E2684		1240.547	11414.5	9.201	L15P8B11,L35P78A11
E4107	GP-39	2807.056	24625.66	8.773	O17201,M80927
E4407	G353	247.063	2154.39	8.72	J122D01F1
E1374	4725948 (AL049730) putative Phospholipase D [Arabidops...	615.534	5037.75	8.184	L18P33H09,L35P114C12
E4794	G915	937.549	7666.25	8.177	J126D04F1
E1200	2829919 (AC002291) Unknown protein [Arabidopsis thaliana]	710.493	5686.35	8.003	L18P10H11,L35P112F10
E4111	GP-39	3787.444	28800.72	7.604	O17205,M80927
E1832		2748.09	19700.01	7.169	L28P4E07,L35P119H02
E2109	2052383 (U66345) calreticulin [Arabidopsis thaliana]	5429.877	38102.85	7.017	L20P2H03,L35P92F03
E2126	G348	2589.263	17690.62	6.832	L20P17D07,L35P92A08
E4570	G1043	1669.306	11210.13	6.715	J123D08F1
E3173	3241945 (AC004625) unknown protein [Arabidopsis thaliana]	1469.642	9650.99	6.567	L15P4D01,L35P101E05
E2111	2739381 (AC002505) putative patatin [Arabidopsis thali...	3904.479	25296.03	6.479	L20P2H07,L35P92F05
E6736	3851530 (AF065435) nodulin [Glycine max]	569.135	3662.91	6.436	J46B06F1
E4610	G503	555.878	3455.08	6.216	J124F04F1
E501	4115383 (AC005967) receptor-like protein kinase [Arabi...	3133.282	19228.29	6.137	L17P32C01,L35P85C01
E4109	GP-39	4114.51	25186.95	6.121	O17203,M80927
E1460	3451056 (AL031326) serine/threonine kinase - like prot...	1487.875	9078.35	6.102	L18P8F11,L35P115B08
E3727	3036808 (AL022373) DnaJ-like protein [Arabidopsis thal...	2243.568	13328.56	5.941	L17P15D06,L35P107B10
E1949	4539301 (AL049480) putative mitochondrial protein [Ara...	1708.963	10020.2	5.863	L18P4E04,L35P90C11
E4918	G348	523.482	2888.43	5.518	J127F10F1
E3736	1695719 (D89342) luminal binding protein [Arabidopsis ...	3477.807	18695.42	5.376	L17P16D02,L35P107D08
E1525	2160152 (AC000375) ESTs gb U75592.gb T13956.gb T43869 ...	533.935	2845.95	5.33	L20P7B02,L35P116E01
E4664	G553	1100.709	5843.25	5.309	J124F11F1
E1559	2244869 (Z97337) hypothetical protein [Arabidopsis tha...	742.606	3857.41	5.194	L20P2E02,L35P116B11
E2788	1523796 (X97864) cytochrome P450 [Arabidopsis thaliana]	2259.751	11734.11	5.193	L23P5G04,L35P97C07
E4844	G1006	780.45	4039.75	5.176	J126E09F1

E4630	G19	1624.861	8339.05	5.132	J124B10F1
E6869		720.814	3617.95	5.019	J47G05F1
E1235		1960.756	9778.73	4.987	L18P27D06,L35P113D03
E1909		4884.253	24309.01	4.977	L18P5C02,L35P90E01
E1454	3688186 (AL031804) putative protein [Arabidopsis thaliana] ... +3 676 1	2203.476	10854.56	4.926	L18P6F12,L35P115A08
E3884	480907 peroxidase (EC 1.11.1.7) - Arabidopsis thaliana ... +3 493 2	2005.276	9863.7	4.919	L17P27B07,L35P109H01
E1491	3193289 (AF069298) similar to several small proteins (... +1 415 4	2260.233	10986.97	4.861	L20P16E07,L35P115G09
E1424	2224933 (AF004216) ethylene-insensitive3 [Arabidopsis thaliana] ... +2 486	1275.625	6183.14	4.847	L20P11E03,L35P115D02
E4586	G1427	342.165	1649.61	4.821	J123H08F1
E4444	G371	414.709	1998.31	4.819	J122C09F1
E5067		627.912	2947.53	4.694	J129A09F1
E1450	2914705 (AC003974) putative disease resistance protein ... +1 285	716.536	3349.54	4.675	L20P17C01,L35P115H04
E567		1732.19	8081.93	4.666	L17P37H03,L35P85F08
E1867	2435406 (U83490) thaumatin-like protein [Arabidopsis thaliana] ... +2 573 1	996.241	4568.44	4.586	L28P1F06,L35P119F07
E1209	1495269 (X97829) product similar to ccr protein, Citrus ... +1 387 1	1892.716	8257.91	4.363	L18P17E02,L35P112H07
E2084	4587610 (AC006951) putative indole-3-glycerol phosphatase ... +2 413	3302.844	14378.33	4.353	L20P17H02,L35P92B02
E2086		2913.592	12600.34	4.325	L20P1A01,L35P92B04
E4827	G186	230.662	991.04	4.296	J126C05F1
E2990		3159.116	13532.76	4.284	L28P3C02,L35P98E08
E5030	G789	1248.951	5339.89	4.276	J128D10F1
E4014	CATALASE 3	1407.248	5975.97	4.247	L15P9C05F1
E1211	4455208 (AL035440) putative protein [Arabidopsis thaliana] ... +2 486 1	1752.529	7401.57	4.223	L18P17G07,L35P112H09
E1080		2335.298	9794.7	4.194	L17P41F08,L35P111D04
E3703	2880054 (AC002340) putative cytochrome P450 [Arabidopsis thaliana] ... +3 7	2149.533	9003.91	4.189	L17P16C08,L35P107D06
E617		1230.038	5111.19	4.155	L17P6D01,L35P86F04
E6768		1600.453	6642.4	4.15	J46F06F1
E1289	2281631 (AF003096) G19 AP2 domain containing protein RAP2 ... +2	3059.227	12668.69	4.141	L18P29A07,L35P113E09
E4108	GP-39	598.122	2457.8	4.109	O17202.M80927
E2551		4274.989	17375.04	4.064	L22P8E01,L35P96B05
E5134	2117612 catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana +3 840 1	2836.449	11520.22	4.061	J129B06F1
E4675	G629	697.491	2810.87	4.03	J124H05F1
E1546		658.495	2650.28	4.025	L21P9B05,L35P116H04
E1456	1172599 PROTEASOME COMPONENT C5 (MULTICATALYTIC ENZYME) ... +2 570	1054.811	4228.73	4.009	L18P6H10,L35P115A10
E1769	871782 (L43081) pEARL1 4 gene product [Arabidopsis thaliana] ... +2 570	895.597	3590.37	4.009	L23P12E04,L35P118E11
E2251		1912.913	7652.44	4	L22P11C08,L35P93F07
E3416		1716.318	6859.17	3.996	L15P9B06,L35P103C04
E76	4678328 (AL049658) aldehyde dehydrogenase (NAD+)-like ... +2 1	3385.029	13472.7	3.98	L16P7G07,L35P80D07

E2682	3702964 (AF079485) rac GTP binding protein Arac10 [Ara... +1 49	1914.858	7589.12	3.963	L15P8B04,L35P78A09
E1220	2894563 (AL021890) putative protein [Arabidopsis thali... +1 293 2	1255.343	4933.99	3.93	L18P1D03,L35P113A06
E1011	4263818 (AC006067) unknown protein [Arabidopsis thaliana] +3 11	1334.817	5245.54	3.93	L17P37F07,L35P110H04
E2743	3152621 (AC004482) cold acclimation protein WCOR413-li... +2 41	1367.015	5334.48	3.902	L23P3D08,L35P97C04
E1704	3928099 (AC005770) unknown protein [Arabidopsis thaliana] +2 31	1605.344	6260.1	3.9	L22P7D12,L35P118B06
E2037	3395425 G915 (AC004683) putative DNA binding protein [Arabi... +	4678.14	18204.85	3.891	L20P11B02,L35P91B09
E1847	G899	2225.184	8566.58	3.85	L24P1C01,L35P119B11
E3296	2781394 (U70424) O-methyltransferase 1 [Arabidopsis th... +3 325	1894.076	7254.63	3.83	L34P4G06,L35P120D08
E2211	3281848 (AL031004) putative protein [Arabidopsis thali... +3 185 1	1924.593	7236.45	3.76	L22P12B01,L35P93G03
E3851	3894183 (AC005662) calmodulin-like protein [Arabidopsi... +3 462	1107.318	4154.28	3.752	L17P21G01,L35P109B04
E3531	3168840 (U88711) copper homeostasis factor [Arabidopsi... +1 541	2883.33	10769.87	3.735	L16P2B04,L35P104F07
E4014	CATALASE 3	1834.619	6839.57	3.728	L15P9C05F1
E1455	128188 NITRATE REDUCTASE 2 (NR2) >pir RDMUNH nitrate ... +	4747.021	17496.84	3.686	L18P6G08,L35P115A09
E2737	4115914 (AF118222) contains similarity to Iron/Ascorbate family of c	2668.747	9816.58	3.678	L23P2E08,L35P97B04
E4575	G1275	425.378	1554.78	3.655	J123F05F1
E1843		2260.903	8233.04	3.641	L24P12H04,L35P119B07
E3579	1705677 CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >pir S.	3195.846	11578.25	3.623	L16P6A02,L35P105G10
E146	1361986(G364) finger protein 2 - Arabidopsis thaliana >gj 79... +1	846.224	3058.56	3.614	L17P16D07,L35P81G05
E2547	3047119 (AF058919) No definition line found [Arabidops... +2 727	1762.811	6332.48	3.592	L22P8C12,L35P96B01
E4349	G921	1639.61	5889.22	3.592	J121G09F1
E4659	G511	1084.072	3890.93	3.589	J124F05F1
E3261	2894599 (AL021889) putative protein [Arabidopsis thali... +1 587 2	3872.867	13888.17	3.586	L34P3G03,L35P120D03
E2977	3341679 (AC003672) dynamin-like protein phragmoplastin... +1 26	2543.148	9070.67	3.567	L28P1D10,L35P98C07
E5027	G528	3620.223	12858.98	3.552	J128D05F1
E2807		813.658	2888.7	3.55	L24P12H08,L35P97F11
E1078	231683 CALNEXIN HOMOLOG PRECURSOR >pir JN0597 calnex	2199.992	7778.4	3.536	L17P41E07,L35P111D01
E3084		2668.719	9430.95	3.534	L34P1H02,L35P99F06
E3570		6848.899	24180.65	3.531	L16P5B04,L35P105C07
E2805		1883.199	6610.18	3.51	L24P12E05,L35P97F09
E3702	3297815 (AL031032) putative protein [Arabidopsis thali... +1 219 2	1897.239	6642.75	3.501	L17P16C03,L35P107D04
E1465		1369.385	4790.79	3.498	L20P10A03,L35P115C07
E1472	1707013 (U78721) Brassica napus hypothetical protein 2... +3 346	1162.838	4058.27	3.49	L20P11G08,L35P115D08
E1106	2129634 lectin-like protein - Arabidopsis thaliana >em... +1 426 3.	4574.824	15918.3	3.48	L17P3E09,L35P111B08
E308	2828292 (AL021687) neoxanthin cleavage enzyme-like pro... +3 11	1140.677	3961.46	3.473	L17P21B07,L35P83B06
E4839	4544394 (AC007047) hypothetical protein [Arabidopsis t... +3 631	670.619	2315.81	3.453	J126D07F1
E1537	3777449 (AJ011844) ppc2 [Solanum tuberosum] +1 433 2	1762.811	6059.39	3.437	L21P2C11,L35P116G01
E1423	1944132 (AB002560) CUC2 [Arabidopsis thaliana] +3 491 1	1136.353	3900.41	3.432	L20P11C07,L35P115D01

E3829	4507433 testis enhanced gene transcript >sp P55061 TEG... +3 16	8167.193	27999.71	3.428	L17P1G02,L35P108F09
E1155	4531445 (AC006224) unknown protein [Arabidopsis thaliana] +3 51	819.597	2808.55	3.427	L18P10D05,L35P112F01
E3554	4185509 (AF102821) actin depolymerizing factor 3 [Arab... +3 637	3894.952	13335.28	3.424	L16P5E08,L35P105E05
E3463	3123188 CATALASE 3 >gj 2347178 (U43147) catalase 3 [Ar... +2	10783.952	36889.66	3.421	L15P9C05,L35P103C09
E6297	584825 B2 PROTEIN >pir S32124 B2 protein - carrot >e... +2 240	1003.134	3426.68	3.416	J39G07F1
E4758	G899	325.782	1111.97	3.413	J125C08F1
E1458	1708924 MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (N	2836.204	9654.93	3.404	L18P7C03,L35P115A12
E2979	2191147 (AF007269) A_IG002N01.26 gene product [Arabido... +1	3705.665	12564.45	3.391	L28P1E05,L35P98C09
E2382	2213626 (AC000103) F21J9.18 [Arabidopsis thaliana] +2 468	1547.983	5230.96	3.379	L22P3G11,L35P95E05
E1593		1443.978	4869.88	3.373	L22P10A10,L35P116H09
E2309		2710.916	9096.95	3.356	L22P21D08,L35P94G05
E2056	1168257 ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC IS	1862.775	6206.1	3.332	L20P14B07,L35P91E10
E4465	G5	1072.76	3554.76	3.314	J122E08F1
E5114	G915	1379.932	4557.12	3.302	J129G01F1
E4519	G1009	475.223	1567.52	3.298	J123D03F1
E3685	121902 HISTONE H1.1 >pir HSMU11 histone H1.1 - Arabi... +3 3	1643.632	5397.49	3.284	L17P14A11,L35P107A04
E3285	3805847 (AL031986) putative protein [Arabidopsis thali... +1 246 1	1305.509	4281.8	3.28	L34P1D11,L35P120B09
E4663	G525	649.667	2127.73	3.275	J124F07F1
E2533		559.523	1823.36	3.259	L15P7B11,L35P77G11
E6225	3075398 (AC004484) unknown protein [Arabidopsis thaliana] +3 7;	1000.008	3255.42	3.255	J39D01F1
E2059	2924777 (AC002334) putative receptor protein kinase [A... +2 116	3441.691	11162.86	3.243	L20P14E08,L35P91F07
E1287	4587989 (AF085279) hypothetical Cys-3-His zinc finger ... +3 255	5228.419	16951.09	3.242	L18P28C09,L35P113E07
E1594	4559366 (AC006585) putative tyrosine transaminase [Ara... +2 33	1414.934	4575.24	3.234	L22P10B04,L35P116H10
E3420	4689436 (AF143096) peptidyl-prolyl cis-trans isomerase... +3 224	2522.441	8136.57	3.226	L15P9E08,L35P103D02
E4905	G6	2092.295	6748.6	3.225	J127D04F1
E4514	G986	228.387	736.52	3.225	J123C12F1
E1985		660.27	2127.74	3.223	L18P8F06,L35P91A05
E2968		3470.414	11167.18	3.218	L24P5H11,L35P98A10
E3726	3249099 (AC003114) EST gb T21244 comes from this gene.... +2	1495.23	4798.31	3.209	L17P15D01,L35P107B09
E3922	1086263 TMV resistance protein N - tobacco (Nicotiana ... +3 262	921.28	2949.03	3.201	L17P25H03,L35P109F09
E1428	1946371 (U93215) regulatory protein Viviparous-1 iso... +3 299 ;	1569.238	4957.17	3.159	L20P11G03,L35P115D06
E3468	G654	1869.904	5903.25	3.157	L15P9G04,L35P103D08
E1348	3021270 (AL022347) serine/threonine kinase -like prote... +3 662	1978.555	6236.2	3.152	L18P4H10,L35P114G03
E3240	1707011 (U78721) auxin-repressed protein isolog [Arabi... +3 529	5770.342	18128.96	3.142	L15P5A11,L35P101H12
E5069	G189	909.864	2853.61	3.136	J129A10F1
E3344	2760324 (AC002130) F1N21.9 [Arabidopsis thaliana] +3 776	559.957	1756.11	3.136	L15P7G08,L35P102G01
E670	3548818 (AC005313) unknown protein [Arabidopsis thaliana] +2 6;	2095.987	6571.1	3.135	L17P7B05,L35P86G09

E1265	1703220	AIG2 PROTEIN >gi 127806 (U40857)	AIG2 [Arabid...	+2	2627.41	8225.68	3.131	L18P1G08,L35P113A09
E2428	2191140	(AF007269)	contains weak similarity to MYB-rel...	+2 440	1330.285	4160.31	3.127	L22P5H06,L35P95F08
E4377	G528				1631.31	5079.38	3.114	J121D06F1
E4518	G1050				743.748	2314.46	3.112	J123D10F1
E1871					1370.971	4245.3	3.097	L28P1G06,L35P119F11
E4635	G209				365.817	1129.86	3.089	J124C05F1
E5031	G895				1119.433	3447.93	3.08	J128D07F1
E1714					1495.523	4599.98	3.076	L22P9A11,L35P118D04
E2578	4455220	(AL035440)	putative aconitase [Arabidopsis tha...	+3 194	2510.27	7670.43	3.056	L23P14C08,L35P96G03
E3748	4324714	(AF110771)	ammonium transporter [Arabidopsis t...	+1 3	7739.662	23646	3.055	L17P17F09,L35P107H08
E4405	G427				1407.645	4299.92	3.055	J122C03F1
E2378					3058.066	9334.48	3.052	L22P3E03,L35P95E01
E764	3608142	(AC005314)	putative hin1 [Arabidopsis thaliana]	+1 171	3570.425	10865.12	3.043	L18P15H06,L35P87G08
E1796					1712.654	5200.44	3.036	L24P10B02,L35P119B02
E6637	584825	B2 PROTEIN >pir S32124 B2 protein - carrot	>e... +3 69£	1255.315	3811.66	3.036	J45F01F1	
E4450	G354				375.221	1139.13	3.036	J122C12F1
E2099					2116.155	6408.84	3.029	L20P2A10,L35P92D05
E2546	3080393	(AL022603)	NADH dehydrogenase like protein [Ar...	+3 6	1175.283	3555.06	3.025	L22P8B02,L35P96A06
E2137	3164222	(AB008518)	RMA1 [Arabidopsis thaliana]	>gi 420... +1 41	12630.59	38191.51	3.024	L20P1E10,L35P92C07
E6877	1352347	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)	>pir ...	1953.354	5889.43	3.015	J47H05F1	
E4666	G554				409.468	1229.85	3.004	J124F12F1
E680					569.229	1707.68	3	L17P7G10,L35P87A01
E1555	2914703	(AC003974)	unknown protein [Arabidopsis thaliana]	+3 41	1916.407	5743.43	2.997	L20P2A07,L35P116B07
E1237					542.423	1625.45	2.997	L18P27E03,L35P113D05
E3734					4016.132	12034.73	2.997	L17P16A04,L35P107C11
E250	2618727	(U49075)	IAA19 [Arabidopsis thaliana]	+2 334 1	3276.623	9805.89	2.993	L17P17D08,L35P82A07
E3886	2642215	(AF030386)	NOI protein [Arabidopsis thaliana]	+1 298	1491.453	4458.27	2.989	L17P27C06,L35P109H03
E2139	4249410	(AC006072)	unknown protein [Arabidopsis thaliana]	+1 3	3473.87	10350.6	2.98	L20P1F03,L35P92C09
E1807	4741198	(AL049746)	putative protein [Arabidopsis thali...	+2 467 £	1978.772	5894.73	2.979	L24P5F09,L35P119D01
E4537	G1273				127.365	379.04	2.976	J123F04F1
E1583	3695023	(AF055850)	unknown [Arabidopsis thaliana]	+2 502	5608.834	16642.52	2.967	L21P2A11,L35P116F11
E4797	G1216				345.554	1021.94	2.957	J126E03F1
E3729	3702339	(AC005397)	unknown protein [Arabidopsis thaliana]	+2 1	5406.168	15949.1	2.95	L17P15E02,L35P107B12
E2387	2191176	(AF007270)	Similar to SRF-type transcription f...	+3 282	1821.522	5360.25	2.943	L22P5F07,L35P95F04
E4560	G787				479.604	1408.03	2.936	J123B06F1
E1992					2558.586	7489.53	2.927	L20P10C03,L35P91B06
E1414	4263710	(AC006223)	putative pur-alpha transcriptional ...	+3 528	2391.809	6994.71	2.924	L18P7G02,L35P115B04

At408-Methylenetetra-24-his

EID	COMMENT	(0.928)CY5	CY5/(0.928)METAROV	METACOL	ROW
E840	4454029 (AL035394) tyrosine transaminase like protein ... +3	396	14.853	2	4
E4218		605.059	7.787	3	2
E5356	3319350 (AF077407) No definition line found [Arabidops... +3	894	5.285	3	1
E6937	3319350 (AF077407) No definition line found [Arabidops... +3	539	5.049	1	1
E281	2746341 (AF037590) ATA27 [Arabidopsis thaliana] +3	330	4.591	3	2
E2230	1076442 beta-glucosidase (EC 3.2.1.21) - rape >emb CAA... +2	421	4.498	3	3
E808	2832649 (AL021710) adenylosuccinate lyase - like prote... +2	250	4.379	4	4
E2202		2046.401	4.292	1	3
E986	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ2	6062.818	4.234	3	2
E4143	A.thaliana beta tubulin 1	766.279	4.085	2	3
E132		1292.022	4.084	1	1
E436		1632.976	3.944	4	4
E3566	417381 NITRILASE 1 >pir S22398 nitrilase (EC 3.5.5.1... +2	530	3.838	1	1
E4145	A.thaliana beta tubulin 1	1470.04	3.807	2	3
E5358		2935.026	3.799	3	1
E4220	G222	775.221	3.778	3	2
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th... +2	564	3.766	2	2
E4147	A.thaliana beta tubulin 1	10473.74	3.718	2	3
E6413	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ2	1589.158	3.581	4	2
E6415	585421 LIPOXYGENASE, CHLOROPLAST PRECURSOR >pir JQ2	2407.937	3.545	4	4
E6978	3319350 (AF077407) No definition line found [Arabidops... +2	553	3.537	3	3
E4227		619.854	3.306	3	4
E234	4468813 (AL035601) putative protein [Arabidopsis thali... +3	555	3.292	3	2
E2649	3785997 (AC005499) putative annexin [Arabidopsis thali... +1	595	3.288	1	4
E4217	G40	265.163	3.182	1	4
E4267	G256	566.64	3.167	3	2
E4603	G451	1116.462	3.082	2	2
E2167	4455154 (AL033545) extensin - like protein [Arabidopsi... +2	394	3.056	4	2
E4357	G921	948.972	3.052	3	1
E157	2460203 (AF021244) coronatine-induced protein 1 [Arabi... +2	247	3	1	3
E4222		785.526	2.992	1	2
E1220	2894563 (AL021890) putative protein [Arabidopsis thali... +1	293	2.907	1	3
E540	4587542 (AC006577) Belongs to the PF100657 Lipase/Acyl... +3	37	2.875	1	1
E4274		959.008	2.815	1	2
E3334	3319347 (AF077407) No definition line found [Arabidops... +2	447	2.791	1	2
E1783	4589123 (AF126374) At14a protein [Arabidopsis thaliana] +1	566	2.704	3	2

E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	4312.532	11412.41	2.646	1	1	1
E861	4220464 (AC006216) Similar to gb Y09437 myrosinase bin... +1 43	5050.771	13249	2.623	2	2	10
E5430		3574.414	9288.17	2.599	3	1	2
E2513	1170121 GLUTATHIONE S-TRANSFERASE 103-1A >pir S66354 ...	4667.409	12121.77	2.597	3	1	8
E5935		2967.88	7639.68	2.574	2	1	3
E6215		4668.772	11954.27	2.56	1	2	4
E5632	1170034 GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMM)	3558.024	9022.69	2.536	4	1	3
E2656	2062161 (AC001645) jasmonate inducible protein isolog ... +2 261	12343.26	31282.46	2.534	1	2	8
E6980		3561.289	8983.47	2.523	3	3	7
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	3166.972	7965.66	2.515	1	2	1
E6973		2406.546	6047.09	2.513	1	1	7
E4540	G1356	1045.123	2619.77	2.507	2	1	20
E6578	2244888 (Z97338) similarity to cytochrome P450 [Arabid... +2 290	2870.309	7170.28	2.498	3	3	6
E5447	4056465 (AC005990) F5O8.40 [Arabidopsis thaliana] +3 396	1478.472	3629.11	2.455	3	3	3
E6417		2219.985	5444.37	2.452	4	2	4
E159		2672.868	6521.4	2.44	1	3	8
E370		350.109	848.86	2.425	2	3	9
E1594	4559366 (AC006585) putative tyrosine transaminase [Ara... +2 335	2083.318	5008	2.404	4	4	18
E1493	2062164 (AC001645) jasmonate inducible protein isolog ... +1 555	10793.82	25838.11	2.394	2	1	18
E2232	2924509 (AL022023) subtilisin proteinase - like [Arabi... +3 277 7.5	7939.706	18747.73	2.361	3	3	12
E1753	4388726 (AC006413) putative 12-oxophytodienoate-10,11-... +1 52	4180.419	9862.21	2.359	1	2	18
E4257	G210	664.256	1542.93	2.323	1	4	22
E741	3914996 PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR	8653.151	20097.13	2.323	2	3	10
E3397	4580920 (AF113545) vacuole-associated annexin VCaB42 [... +1 3	5872.073	13557.76	2.309	3	2	15
E4272	G412	397.248	916.71	2.308	1	4	22
E3115		19656.46	45319.03	2.306	4	1	13
E2472		4924.585	11320.4	2.299	1	3	8
E5592		1941.892	4448.39	2.291	2	1	2
E6535	2129516 1-aminocyclopropane-1-carboxylate oxidase homo... +2 1	1015.543	2320.32	2.285	1	1	5
E5432	3193290 (AF069298) contains similarity to a protein ki... +1 415 7.0	1887.685	4282.93	2.269	1	1	2
E6340		1764.57	3978.9	2.255	4	3	5
E3332	2062161 (AC001645) jasmonate inducible protein isolog ... +1 671	18236.58	41042.81	2.251	1	2	14
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR	3828.464	8588.66	2.243	2	2	1
E1999		5222.871	11707.85	2.242	4	1	11
E5708	3885331 (AC005623) putative cytochrome p450 protein [A... +2 26	4947.283	11073.51	2.238	4	2	2
E1693	4468807 (AL035601) cytochrome P450 monooxygenase-like ... +3	7253.346	16025.03	2.209	1	2	18
E6943	2642444 (AC002391) putative cytochrome P450 [Arabidops... +2 5	1268.555	2799.08	2.207	3	3	7

E3920	4115377 (AC005967) unknown protein [Arabidopsis thaliana] +1	26	4558.216	10061.95	2.207	3	1	16
E5609	2129755 tryptophan synthase (EC 4.2.1.20) alpha chain ... +1	561	3697.168	8108.17	2.193	2	1	2
E6255	2244889 (Z97338) similarity to cytochrome P450 [Arabid...	+3 228	1645.61	3606.27	2.191	3	4	4
E4767	G7		707.87	1549.26	2.189	3	1	21
E4226			310.029	678.33	2.188	3	2	22
E2880	3820648 (Y12636) allene oxide synthase [Arabidopsis th...	+2 564	5628.959	12298.63	2.185	4	3	7
E6419			1363.324	2955.49	2.168	4	4	4
E283	4115929 (AF118222) similar to the subtilase family of ... +2	386 3.5	3887.903	8406.49	2.162	3	2	9
E2477	4510339 (AC006921) putative ABC transporter protein [A...	+1 621	6678.729	14414.78	2.158	3	1	8
E790	4734007 (AC007178) hypothetical protein [Arabidopsis t...	+3 340	3800.266	8174.74	2.151	2	4	10
E3168	4468044 (X73587) catechol O-methyltransferase [Vanilla...	+1 304	14742.91	31541.88	2.139	3	3	14
E2698	629602 probable imbibition protein - wild cabbage >em...	+1 256 4	7844.019	16760.76	2.137	3	2	7
E2692	1708463 IAA-AMINO ACID HYDROLASE >gil887785 (U23794) l...	+ 2062.522	4351.95	2.11	1	2	2	7
E1869	2262177 (AC002329) hypothetical protein similar to T18...	+3 337 1	1612.18	3393.53	2.105	4	1	19
E6635	2829898 (AC002311) Hypothetical protein [Arabidopsis t...	+2 594	489.568	1024.92	2.094	1	4	5
E1962			4653.505	9668.86	2.078	1	4	11
E4000	BGL2		9621.166	19941.79	2.073	2	2	1
E2493			1270.596	2618.56	2.061	1	1	7
E1759			7534.63	15510.94	2.059	3	2	18
E4000	BGL2		8221.509	16922.77	2.058	2	1	1
E4015	jasmonate inducible protein		6181.416	12646.16	2.046	4	3	1
E4356	G993		2801.262	5728.43	2.045	3	1	20
E5608	4581500 (AL034352) putative oxalyl-CoA decarboxylase [...]	+1 93	4182.265	8520.2	2.037	2	1	2
E6556			952.126	1937.51	2.035	1	3	5
E5360	3128185 (AC004521) unknown protein [Arabidopsis thaliana]	+2 25	1970.489	4000.44	2.03	1	1	2
E6342	3319340 (AF077407) contains similarity to E. coli cati...	+1 187 5.9	1478.639	2998.26	2.028	2	1	4
E2533			1268.852	2560.21	2.018	1	1	8
E5388	3281849 (AL031004) methyltransferase - like protein [A...	+3 460 2	2819.618	5678.53	2.014	3	1	2
E4000	BGL2		8079.555	16254.56	2.012	1	2	1
E1918			8752.048	17603.95	2.011	3	4	11
E1654	1762933 (U66263) tumor-related protein [Nicotiana taba...	+3 178	8542.279	17137.85	2.006	3	3	18
E5868	2062157 (AC001645) jasmonate inducible protein isolog ...	+3 886	2441.033	4890.12	2.003	1	4	3
E5232	1620371 (Y08782) peroxidase ATP23a [Arabidopsis thaliana]	+1 7C	2499.636	4996.33	1.999	4	2	7
E6353			1493.74	2984.13	1.998	4	1	4
E5182	2062161 (AC001645) jasmonate inducible protein isolog ...	+1 687	6163.866	12316.41	1.998	4	2	7
E2153			3758.09	7494.53	1.994	2	2	11
E4857	G22		538.358	1073.05	1.993	3	4	21

E5229	3759184 (AB018441) phi-1 [Nicotiana tabacum]	+3	182	2.C	2642.593	5267.75	1.993	2	2	7
E4407	G353				1156.283	2298.5	1.988	3	2	19
E5665					2837.362	5636.47	1.987	4	2	2
E5558	1531760 (X97075) proline oxidase [Arabidopsis thaliana]	+1	265	3	2010.597	3991.01	1.985	4	1	2
E5223	1403134 (X98453) peroxidase [Arabidopsis thaliana]	+3	485	1.	2296.018	4536.75	1.976	4	4	6
E2444	2578440 (X67425) pectinesterase [Pisum sativum]	+1	147	2.	5154.649	10141.33	1.967	4	3	12
E4215	G25				526.179	1034.51	1.966	1	4	22
E6617	2062158 (AC001645) jasmonate inducible protein isolog ...	+1	573		6129.129	12032.62	1.963	1	2	5
E2449	3152575 (AC002986) Similar to cytochrome P450tyr gb U3...	+2	18		1779.568	3490.09	1.961	1	1	7
E4056	PUTATIVE TRYPSIN INHIBITOR T01O24.25 PRECURSOR				3563.413	6981.46	1.959	2	1	1
E5556					1888.928	3664.71	1.94	4	1	2
E5433					2023.49	3925.95	1.94	1	3	2
E6453					893.096	1730.51	1.938	2	2	5
E5376	2213583 (AC000348) T7N9.3 [Arabidopsis thaliana]	+2	138	4	3509.178	6795.64	1.937	1	1	2
E2259	4388826 (AC006528) hypothetical protein [Arabidopsis t...	+1	313	3	5777.452	11192.55	1.937	1	1	12
E5640	2827524 (AL021633) predicted protein [Arabidopsis thal...	+2	100	3	1826.633	3536.2	1.936	2	1	2
E4345	G867				4834.983	9357.07	1.935	3	1	20
E5710	2829927 (AC002291) Unknown protein [Arabidopsis thaliana]	+2	82		2456.18	4727.44	1.925	4	2	2
E6344	3319340 (AF077407) contains similarity to E. coli cati...	+3	172	2.0	1316.844	2531.77	1.923	2	3	4
E4000	BGL2				9295.127	17876.85	1.923	1	1	1
E6580	4455239 (AL035523) abscisic acid-induced-like protein ...	+1	160	5	2055.992	3943.99	1.918	3	3	6
E717	3860163 (AF098962) disease resistance protein RPP1-WsA...	+2	1		8219.533	15756.45	1.917	2	3	10
E6357	1742959 (Z71450) CLC-d chloride channel protein [Arabi...	+2	251		2018.472	3853.98	1.909	2	1	4
E1295	452470 (U05218) ATP sulfurylase [Arabidopsis thaliana]	+2	727		13445.38	25668.72	1.909	3	1	18
E4015	jasmonate inducible protein				5557.416	10581.41	1.904	3	3	1
E6475	3080373 (AL022580) putative protein [Arabidopsis thali...	+3	398	1.	1587.869	3009.22	1.895	4	2	4
E6646	3164144 (D78607) cytochrome P450 monooxygenase [Arabid...	+1			1698.138	3217.31	1.895	1	2	6
E6933	3522935 (AC004411) putative alcohol dehydrogenase [Ara...	+1	58		2374.517	4499.76	1.895	1	1	7
E5465	4587529 (AC007060) Strong similarity to F19I3.2 gl 303...	+1	338	6	1079.61	2045.15	1.894	1	2	2
E2478	4432856 (AC006300) putative 2A6 protein [Arabidopsis t...	+1	125		9302.381	17619.53	1.894	3	3	8
E2950					2629.198	4977.57	1.893	3	4	13
E2396	1076261 beta-fructofuranosidase (EC 3.2.1.26) - red go...	+2	231	5	5303.551	10014.84	1.888	4	1	12
E6975	4262181 (AC005508) 37496 [Arabidopsis thaliana]	+2	694	2.	1556.397	2935.39	1.886	1	1	7
E3160	2286069 (U72155) beta-glucosidase [Arabidopsis thaliana]	+1	777		19083.13	35984.08	1.886	1	3	14
E6710					2004.438	3776.64	1.884	2	1	5
E800					3948.593	7437.16	1.883	2	4	10
E4224	G393				956.68	1799.49	1.881	1	2	22

Summary of Overexpressor G28, Family AP2

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G28 corresponds to *AtERF1* (GenBank accession number AB008103) (Fujimoto et al., 2000). G28 appears as gene AT4g17500 in the annotated sequence of Arabidopsis chromosome 4 (AL161546.2).

AtERF1 has been shown to have GCC-box binding activity [some defense-related genes that are induced by ethylene were found to contain a short cis-acting element known as the GCC-box: AGCCGCC (Ohme-Takagi and Shinshi, 1990)]. Using transient assays in Arabidopsis leaves, AtERF1 was found to be able to act as a GCC-box sequence specific transactivator (Fujimoto et al., 2000).

AtERF1 expression has been described to be induced by ethylene (two- to three-fold increase in *AtERF1* transcript levels 12 h after ethylene treatment) (Fujimoto et al., 2000). In the *ein2* mutant, the expression of *AtERF1* was not induced by ethylene, suggesting that the ethylene induction of *AtERF1* is regulated under the ethylene signaling pathway (Fujimoto et al., 2000). *AtERF1* expression was also induced by wounding, but not by other abiotic stresses (such as cold, salinity, or drought) (Fujimoto et al., 2000).

It has been suggested that AtERFs, in general, may act as transcription factors for stress-responsive genes, and that the GCC-box may act as a cis-regulatory element for biotic and abiotic stress signal transduction in addition to its role as an ethylene responsive element (ERE) (Fujimoto et al., 2000), but there is no data available on the physiological functions of *AtERF1*.

Mendel Discoveries

The function of G28 was analyzed at Mendel using transgenic plants in which this gene was expressed under the control of the 35S promoter. G28 overexpressing lines are more tolerant to infection with a moderate dose of the fungal pathogen *Erysiphe orontii*. G28 overexpression does not seem to have detrimental effects on plant growth or vigor, since plants from most of the lines are morphologically wild-type. In addition, no difference was detected between those lines and the corresponding wild-type controls in all the biochemical assays that were performed.

G28 is ubiquitously expressed, and it is not significantly induced under any of the conditions tested (which did not include ethylene treatment).

Closely Related Genes from Other Species

The non-Arabidopsis gene most closely related to G28 is an AP2-related transcription factor gene from *Mesembryanthemum crystallinum* (GenBank accession number AF245119), for which no functional information is available. Conversely, G28 is the Arabidopsis gene most closely related to *Mesembryanthemum* AF245119. Similarity extends between the conserved AP2 domain, which is nearly 100% identical between these two proteins, raising the possibility that the two genes are orthologs.

Utilities

G28 transgenic plants have an altered response to the fungal pathogen *Erysiphe orontii*, in that those plants are more tolerant to that pathogen. Therefore, G28 could be used to manipulate the defense response in order to generate

pathogen-resistant plants.

References

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Keywords

Disease, Erysiphe

Knockout Status

KO DNA insertion not identified

Plasmid ID P174

Cloning Vector pMEN20

Cloning Site NA

Source DNA L22P3E10

Bacterial Strain DH5a

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Patent Information

Disease-Induced Polynucleotides, 3/22/00

Fri Aug 11 10:24:00 PDT 2000

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